



10051909 Sequence Listing.txt

SEQUENCE LISTING

<110> Helentjaris, Tim  
<120> Plant Sugar Transport Proteins  
<130> 2119-4263 (BB1163 US CIP)  
<140> 10/051,909  
<141> 2002-01-17  
<160> 56  
<170> Microsoft Office 97  
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<222> (944)

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aaaa						2824

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Lys Lys Glu Phe Asn Leu Gln Ser Glu Pro Leu Ile Glu Gly Leu Ile  
35 40 45  
Val Ala Met Phe Leu Ile Gly Ala Thr Val Ile Thr Thr Ser Pro Gly  
50 55 60  
Pro Arg Ala Asp Cys Val Gly Arg Arg Pro Met Leu Val Ala Ser Ala  
65 70 75 80  
Val Leu Tyr Phe Val Ser Gly Leu Val Met Leu Trp Ala Pro Ile Val  
85 90 95

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Tyr Ile Leu Leu Leu Ala Arg Leu Ile Asp Gly Phe Gly Ile Gly Leu  
100 105 110

Ala Val Thr Leu Val Pro Leu Tyr Ile Ser Glu Thr Ala Pro His Arg  
115 120 125

Xaa Ser Trp Gly Xaa Xaa Asn Thr Leu Pro Gln Phe Ile Gly Val Xaa  
130 135 140

Gly Gly Met Phe Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Met  
145 150 155 160

Pro Lys Pro Asp Trp Arg Leu Met Leu Gly Val Leu Ser Ile Pro Ser  
165 170 175

Leu Xaa Tyr Phe Gly Leu Thr Val Phe Tyr Leu Pro Glu Ser Pro Arg  
180 185 190

Trp Leu Val Ser Lys Gly Arg Met Ala Glu Ala Lys Arg Val Xaa Gln  
195 200 205

Arg Leu Arg Gly Arg Glu Asp Val Ser Xaa Glu Xaa Ala Leu Leu Val  
210 215 220

Glu Gly Leu Gly Val Gly Lys Asp Thr Arg Ile Xaa Glu Tyr Ile Ile  
225 230 235 240

Gly Pro Ala Thr Glu Ala Ala Asp Asp Leu Val Thr Asp Gly Asp Lys  
245 250 255

Glu Gln Ile Thr Leu Tyr Gly Pro Glu Glu Gly Gln Ser Trp Ile Ala  
260 265 270

Arg Pro Ser Lys Gly Pro Ile Met Leu Gly Ser Val Leu Ser Leu Ala  
275 280 285

Ser Arg His Gly Ser Met Val Asn Gln Ser Val Pro Leu Met Asp Pro  
290 295 300

Ile Val Thr Leu Phe Gly Ser Val His Glu Asn Met Pro Gln Ala Gly  
305 310 315 320

Gly Ser Met Arg Ser Thr Leu Phe Pro Asn Phe Gly Ser Met Phe Ser  
325 330 335

Val Thr Asp Gln His Ala Lys Asn Glu Gln Trp Asp Glu Glu Asn Leu  
340 345 350

His Arg Asp Asp Glu Glu Tyr Ala Ser Asp Gly Ala Gly Gly Asp Tyr  
355 360 365

Glu Asp Asn Leu His Ser Pro Leu Leu Ser Arg Gln Ala Thr Gly Ala  
370 375 380

Glu Gly Lys Asp Ile Val His His Gly His Arg Gly Ser Ala Leu Ser  
385 390 395 400

Met Arg Arg Gln Ser Leu Leu Gly Glu Gly Gly Asp Gly Val Ser Ser  
405 410 415

Thr Asp Ile Gly Gly Gly Trp Gln Leu Ala Trp Lys Trp Ser Glu Lys  
420 425 430

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Glu Gly Glu Asn Gly Arg Lys Glu Gly Gly Phe Lys Arg Val Tyr Leu  
435 440 445

His Gln Glu Gly Val Pro Gly Ser Arg Arg Gly Ser Ile Val Ser Leu  
450 455 460

Pro Gly Gly Gly Asp Val Leu Glu Gly Ser Glu Phe Val His Ala Ala  
465 470 475 480

Ala Leu Val Ser Gln Ser Ala Leu Phe Ser Lys Gly Leu Ala Glu Pro  
485 490 495

Arg Met Ser Asp Ala Ala Met Val His Pro Ser Glu Val Ala Ala Lys  
500 505 510

Gly Ser Arg Trp Lys Asp Leu Phe Glu Pro Gly Val Arg Arg Ala Leu  
515 520 525

Leu Val Gly Val Gly Ile Gln Ile Leu Gln Gln Phe Ala Gly Ile Asn  
530 535 540

Gly Val Leu Tyr Tyr Thr Pro Gln Ile Leu Glu Gln Ala Gly Val Ala  
545 550 555 560

Val Ile Leu Ser Lys Phe Gly Leu Ser Ser Ala Ser Ala Ser Ile Leu  
565 570 575

Ile Ser Ser Leu Thr Thr Leu Leu Met Leu Pro Cys Ile Gly Phe Ala  
580 585 590

Met Leu Leu Met Asp Leu Ser Gly Arg Arg Phe Leu Leu Leu Gly Thr  
595 600 605

Ile Pro Ile Leu Ile Ala Ser Leu Val Ile Leu Val Val Ser Asn Leu  
610 615 620

Ile Asp Leu Gly Thr Leu Ala His Ala Leu Leu Ser Thr Ile Ser Val  
625 630 635 640

Ile Val Tyr Phe Cys Cys Phe Val Met Gly Phe Gly Pro Ile Pro Asn  
645 650 655

Ile Leu Cys Ala Glu Ile Phe Pro Thr Arg Val Arg Gly Leu Cys Ile  
660 665 670

Ala Ile Cys Ala Phe Thr Phe Trp Ile Gly Asp Ile Ile Val Thr Tyr  
675 680 685

Ser Leu Pro Val Met Leu Asn Ala Ile Gly Leu Ala Gly Val Phe Ser  
690 695 700

Ile Tyr Ala Val Val Cys Leu Ile Ser Phe Val Phe Val Phe Leu Lys  
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Val Pro Glu Thr Lys Gly Met Pro Leu Glu Val Ile Thr Glu Phe Phe  
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Ala Val Gly Ala Lys Gln Ala Ala Ala Lys Ala  
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<212> DNA

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<213> Oryza sativa

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<212> PRT

<213> Oryza sativa

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<223> Xaa = any amino acid

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<222> (130)

<223> Xaa = any amino acid

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		20						25					30			
His	Leu	Gly	Val	Pro	Thr	Ser	Pro	Ser	Arg	Phe	Pro	Ala	Ala	Ser	Leu	
		35					40					45				
Leu	Val	Arg	Gly	Ser	Glu	Ile	Ser	Val	Asp	Glu	Arg	Leu	Gly	Gly	Asn	
	50					55					60					
Xaa	Ser	Pro	Ala	Met	Ala	Gly	Ala	Val	Leu	Val	Ala	Ile	Ala	Ala	Ser	
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Ile Gly Asn Leu Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala  
85 90 95

Val Leu Tyr Ile Lys Lys Glu Phe Asn Leu His Ser Asp Pro Leu Ile  
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Glu Gly Leu Ile Val Ala Met Ser Leu Ile Gly Ala Thr Ile Ile Thr  
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Thr Xaa Ser  
130

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<213> Oryza sativa

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<212> PRT  
<213> Oryza sativa

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Val Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe  
35 40 45

Pro Thr Thr Val Arg Gly Ile Cys Ile Ala Ile Cys Ala Leu Thr Phe  
50 55 60

Trp Ile Gly Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn  
65 70 75 80

Ala Ile Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Val Val Cys Ile  
85 90 95

Leu Ala Phe Leu Phe Val Phe Met Lys Val Pro Glu Thr Lys Gly Met  
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Pro Leu Glu Val Ile Thr Glu Phe Phe Ser Val Gly Ala Lys Gln Ala  
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Lys Glu Asp  
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gcttttcata agtttatttg gaggaagata ttttgaaaca tatgggtttt tttttctttc 2520  
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aaaaaaaaaa aaaaaaaaaa a 2601

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1 5 10 15

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Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Asn Gly Tyr Ile  
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 Lys Lys Asp Leu Ala Leu Gly Thr Thr Met Glu Arg Leu Val Val Gly  
 35 40 45  
 Met Ser Leu Ile Gly Ala Thr Val Ile Thr Thr Cys Ser Gly Pro Ile  
 50 55 60  
 Ala Asp Trp Leu Gly Arg Arg Pro Met Met Ile Ile Ser Ser Val Leu  
 65 70 75 80  
 Tyr Phe Leu Gly Gly Leu Val Met Leu Trp Ser Pro Asn Val Tyr Val  
 85 90 95  
 Leu Cys Leu Ala Arg Leu Leu Asp Gly Phe Gly Ile Gly Leu Ala Val  
 100 105 110  
 Thr Leu Val Pro Val Tyr Ile Ser Glu Thr Ala Pro Ser Glu Ile Arg  
 115 120 125  
 Gly Ser Leu Asn Thr Leu Pro Gln Phe Ser Gly Ser Gly Gly Met Phe  
 130 135 140  
 Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Ser Pro Ala Pro Ser  
 145 150 155 160  
 Trp Arg Leu Met Leu Gly Val Leu Ser Ile Pro Ser Leu Leu Tyr Phe  
 165 170 175  
 Ala Leu Thr Ile Phe Phe Leu Pro Glu Ser Pro Arg Trp Leu Val Ser  
 180 185 190  
 Lys Gly Arg Met Leu Glu Ala Lys Lys Val Leu Gln Arg Leu Arg Gly  
 195 200 205  
 Arg Glu Asp Val Ser Gly Glu Met Ala Leu Leu Val Glu Gly Leu Gly  
 210 215 220  
 Ile Gly Gly Asp Thr Ser Ile Glu Glu Tyr Ile Ile Gly Pro Ala Asp  
 225 230 235 240  
 Asp Val Ala Asp Gly His Glu His Ala Thr Glu Lys Asp Lys Ile Arg  
 245 250 255  
 Leu Tyr Gly Ser Gln Ala Gly Leu Ser Trp Leu Ser Lys Pro Val Thr  
 260 265 270  
 Gly Gln Ser Ser Ile Gly Leu Ala Ser His His Gly Ser Ile Ile Asn  
 275 280 285  
 Gln Ser Met Pro Leu Met Asp Pro Leu Val Thr Leu Phe Gly Ser Ile  
 290 295 300  
 His Glu Lys Leu Pro Glu Thr Gly Ala Arg Gly Ser Met Arg Ser Thr  
 305 310 315 320  
 Leu Phe Pro Asn Phe Gly Ser Met Phe Ser Thr Ala Glu Pro His Ala  
 325 330 335  
 Lys Ile Glu Gln Trp Asp Glu Glu Ser Leu Gln Arg Glu Arg Glu Asp  
 340 345 350

10051909 Sequence Listing.txt

Tyr	Met	Ser	Asp	Ala	Thr	Arg	Gly	Asp	Ser	Asp	Asp	Asn	Leu	His	Ser
		355					360					365			
Pro	Leu	Ile	Ser	Arg	Gln	Thr	Thr	Ser	Leu	Glu	Lys	Asp	Leu	Pro	Pro
	370					375					380				
Pro	Pro	Ser	His	Gly	Ser	Ile	Leu	Gly	Ser	Met	Arg	Arg	His	Ser	Ser
385					390					395					400
Leu	Met	Gln	Gly	Ser	Gly	Glu	Gln	Gly	Gly	Ser	Thr	Gly	Ile	Gly	Gly
				405					410					415	
Gly	Trp	Gln	Leu	Ala	Trp	Lys	Trp	Thr	Asp	Lys	Gly	Glu	Asp	Gly	Lys
			420					425					430		
Gln	Gln	Gly	Gly	Phe	Lys	Arg	Ile	Tyr	Leu	His	Glu	Glu	Gly	Val	Ser
		435					440					445			
Ala	Ser	Arg	Arg	Gly	Ser	Ile	Val	Ser	Ile	Pro	Gly	Glu	Gly	Glu	Phe
	450					455					460				
Val	Gln	Ala	Ala	Ala	Leu	Val	Ser	Gln	Pro	Ala	Leu	Tyr	Ser	Lys	Glu
465					470					475					480
Leu	Ile	Asp	Gly	His	Pro	Val	Gly	Pro	Ala	Met	Val	His	Pro	Ser	Glu
				485					490					495	
Thr	Ala	Ser	Lys	Gly	Pro	Ser	Trp	Lys	Ala	Leu	Leu	Glu	Pro	Gly	Val
			500					505					510		
Lys	His	Ala	Leu	Val	Val	Gly	Val	Gly	Ile	Gln	Ile	Leu	Gln	Gln	Phe
		515					520					525			
Ser	Gly	Ile	Asn	Gly	Val	Leu	Tyr	Tyr	Thr	Pro	Gln	Ile	Leu	Glu	Glu
	530					535					540				
Ala	Gly	Val	Glu	Val	Leu	Leu	Ser	Asp	Ile	Gly	Ile	Gly	Ser	Glu	Ser
545					550					555					560
Ala	Ser	Phe	Leu	Ile	Ser	Ala	Phe	Thr	Thr	Phe	Leu	Met	Leu	Pro	Cys
				565					570					575	
Ile	Gly	Val	Ala	Met	Lys	Leu	Met	Asp	Val	Ser	Gly	Arg	Arg	Gln	Leu
			580					585					590		
Leu	Leu	Thr	Thr	Ile	Pro	Val	Leu	Ile	Val	Ser	Leu	Ile	Ile	Leu	Val
		595					600					605			
Ile	Gly	Ser	Leu	Val	Asn	Phe	Gly	Asn	Val	Ala	His	Ala	Ala	Ile	Ser
	610					615					620				
Thr	Val	Cys	Val	Val	Val	Tyr	Phe	Cys	Cys	Phe	Val	Met	Gly	Tyr	Gly
625					630					635					640
Pro	Ile	Pro	Asn	Ile	Leu	Cys	Ser	Glu	Ile	Phe	Pro	Thr	Arg	Val	Arg
				645					650					655	
Gly	Leu	Cys	Ile	Ala	Ile	Cys	Ala	Leu	Val	Phe	Trp	Ile	Gly	Asp	Ile
			660					665					670		
Ile	Ile	Thr	Tyr	Ser	Leu	Pro	Val	Met	Leu	Gly	Ser	Leu	Gly	Leu	Gly
		675					680					685			

10051909 Sequence Listing.txt

Gly Val Phe Ala Ile Tyr Ala Val Val Cys Phe Ile Ser Trp Ile Phe  
690 695 700

Val Phe Leu Lys Val Pro Glu Thr Lys Gly Met Pro Leu Glu Val Ile  
705 710 715 720

Ser Glu Phe Phe Ser Val Gly Ala Lys Gln Ala Ala Ser Ala Lys Asn  
725 730 735

Glu

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<211> 1692  
<212> DNA  
<213> Glycine max

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gaagcatggc aaatccaagc agtctagtgg accctctagt gaccctcttt ggtagtgtac 180  
atgagaagct cccagaaaca ggaagcacc tttttccaca ctttgggagt atgttcagt 240  
ttgggggaaa tcagccaagg aatgaagatt gggatgagga aagcctagcc agagagggtg 300  
atgattatgt ctctgatgct ggtgattctg atgacaattt gcagagtcca ttgatctcac 360  
gtcaaacaac gagtctggat aaggacatac ctctcatgac ccatagtaac cttgcaagca 420  
tgaggcaagg tagtctttta catggaaatt caggagaacc cactggtagt actgggattg 480  
gtggtggttg gcagctagca tggaaatggt ctgaaagaga gggcccagat ggaaagaagg 540  
aaggtggctt caagagaata tatttacacc aagatgggtg ttctggatct agacgtgggt 600  
ctgtggtttc actccctggc ggtgattttac caactgacag tgagggttgta caggctgctg 660  
ctctggtgag tcagcctgcc ctttataatg aggaccttat gcgtcaacgg ccagttggac 720  
cagctatgat tcatccctct gaaacaattg caaaagggcc aagttggagt gatctttttg 780  
aacctggggg gaagcatgca ttgattgtgg ggggtgggaat gcaaattctt cagcagttct 840  
ctggtataaa tggggtcctc tactatacgc ctcaaattct tgagcaggca ggtgttggtt 900  
atcttctttc aagcctaggg cttggttcta cttcttcac ctttcttatt agtgcggtga 960  
caaccttggt gatgcttcct tgtatagcca ttgccatgag gctcatggat atttcaggca 1020  
gaaggacttt gctgctcagt acaatccccg tcctaatagc agctcttctc atattagtcc 1080  
tggaagtct tgtggatttg ggatccactg caaatgcatc aatctcaacc attagtgtta 1140  
ttgtctatct ctgtttcttt gtcattgggt ttggaccaat tcctaataata ctttgtgcag 1200  
agatcttccc cactcgagtt cgtgggtctc gcattgctat ttgtgccctt accttttgga 1260  
tctgtgatat cattgtcacc tacacactcc cagttatgct caattctgta ggcctcgctg 1320  
gtgttttttg tatttatgct gtcgtgtgct tcatagcatg ggtgtttgtc tttttgaaag 1380  
ttccagaaac caagggcatg ccactggaag tgatcattga gttcttctct gtcggagcaa 1440  
aacagtttga cgatgccaag cacaactgac ccaaggacat gataaattca aagttttgac 1500  
ggtaccttct aattattttc aatctacggc tgtttgaaat tttcccctct tttaaaattt 1560  
tattttctat ttattctctc ttttccgtgg gttgagattg agaaacaaga aactttgttt 1620  
ctgtaaagaa aaatgttcat tttctggttc atttatggaa ctttatatac ttcctaaaaa 1680  
aaaaaaaaaa aa 1692

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<211> 486  
<212> PRT  
<213> Glycine max

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Asp Pro Ser Arg Glu Lys Asp Gln Ile Lys Leu Tyr Gly Pro Glu Gln  
1 5 10 15

Gly Gln Ser Trp Val Ala Arg Pro Val Ala Gly Pro Asn Ser Val Gly  
20 25 30

Leu Val Ser Arg Lys Gly Ser Met Ala Asn Pro Ser Ser Leu Val Asp  
35 40 45

10051909 Sequence Listing.txt

Pro Leu Val Thr Leu Phe Gly Ser Val His Glu Lys Leu Pro Glu Thr  
50 55 60  
Gly Ser Thr Leu Phe Pro His Phe Gly Ser Met Phe Ser Val Gly Gly  
65 70 75 80  
Asn Gln Pro Arg Asn Glu Asp Trp Asp Glu Glu Ser Leu Ala Arg Glu  
85 90 95  
Gly Asp Asp Tyr Val Ser Asp Ala Gly Asp Ser Asp Asp Asn Leu Gln  
100 105 110  
Ser Pro Leu Ile Ser Arg Gln Thr Thr Ser Leu Asp Lys Asp Ile Pro  
115 120 125  
Pro His Ala His Ser Asn Leu Ala Ser Met Arg Gln Gly Ser Leu Leu  
130 135 140  
His Gly Asn Ser Gly Glu Pro Thr Gly Ser Thr Gly Ile Gly Gly Gly  
145 150 155 160  
Trp Gln Leu Ala Trp Lys Trp Ser Glu Arg Glu Gly Pro Asp Gly Lys  
165 170 175  
Lys Glu Gly Gly Phe Lys Arg Ile Tyr Leu His Gln Asp Gly Gly Ser  
180 185 190  
Gly Ser Arg Arg Gly Ser Val Val Ser Leu Pro Gly Gly Asp Leu Pro  
195 200 205  
Thr Asp Ser Glu Val Val Gln Ala Ala Ala Leu Val Ser Gln Pro Ala  
210 215 220  
Leu Tyr Asn Glu Asp Leu Met Arg Gln Arg Pro Val Gly Pro Ala Met  
225 230 235 240  
Ile His Pro Ser Glu Thr Ile Ala Lys Gly Pro Ser Trp Ser Asp Leu  
245 250 255  
Phe Glu Pro Gly Val Lys His Ala Leu Ile Val Gly Val Gly Met Gln  
260 265 270  
Ile Leu Gln Gln Phe Ser Gly Ile Asn Gly Val Leu Tyr Tyr Thr Pro  
275 280 285  
Gln Ile Leu Glu Gln Ala Gly Val Gly Tyr Leu Leu Ser Ser Leu Gly  
290 295 300  
Leu Gly Ser Thr Ser Ser Ser Phe Leu Ile Ser Ala Val Thr Thr Leu  
305 310 315 320  
Leu Met Leu Pro Cys Ile Ala Ile Ala Met Arg Leu Met Asp Ile Ser  
325 330 335  
Gly Arg Arg Thr Leu Leu Leu Ser Thr Ile Pro Val Leu Ile Ala Ala  
340 345 350  
Leu Leu Ile Leu Val Leu Gly Ser Leu Val Asp Leu Gly Ser Thr Ala  
355 360 365  
Asn Ala Ser Ile Ser Thr Ile Ser Val Ile Val Tyr Phe Cys Phe Phe  
370 375 380

10051909 Sequence Listing.txt

Val Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe  
385 390 395 400  
Pro Thr Arg Val Arg Gly Leu Cys Ile Ala Ile Cys Ala Leu Thr Phe  
405 410 415  
Trp Ile Cys Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn  
420 425 430  
Ser Val Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Val Val Cys Phe  
435 440 445  
Ile Ala Trp Val Phe Val Phe Leu Lys Val Pro Glu Thr Lys Gly Met  
450 455 460  
Pro Leu Glu Val Ile Ile Glu Phe Phe Ser Val Gly Ala Lys Gln Phe  
465 470 475 480  
Asp Asp Ala Lys His Asn  
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<212> DNA  
<213> Triticum aestivum

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<222> (421)  
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<220>  
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<222> (434)  
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<400> 11

10051909 Sequence Listing.txt

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gcttctccat	ctcatctcct	tggttgggtc	tctactagag	aggcgcagct	gcagggatcc	180
ttggtggaga	ggaggggaaga	agatgtcggg	tgctgcactg	gtcgcgattg	cggcttccat	240
tggcaatctg	ctgcaggggt	gggacaatgc	caccatcgct	ggtgctgttc	tgtacatcaa	300
gaaggaattc	cagctcgaaa	ataatccgac	tgtggagggg	ctcatcgtgg	catgtcctca	360
tcgggtgcaa	catcatcaca	cattctccgg	gccagtatca	aactgggttg	ccgggcccta	420
ngccatctcc	ttgntttcaa	ntcccaaggg	ctaatacanct	aggcaccaat	gtcaatgtgc	480
gcnccggaac	ctntcaangg	ttggaacggt				510

<210> 12  
 <211> 117  
 <212> PRT  
 <213> Triticum aestivum

<400> 12  
 Gly Gly Ser Arg Gly Ser Glu Gly Gly Val Ala Leu Gly Ser Tyr Leu  
 1 5 10 15  
 Arg Arg Leu Arg Ser Val Leu Ile Tyr Arg Thr Thr Pro Pro His His  
 20 25 30  
 Thr Arg Gly Leu Pro Leu Leu Gly Leu Leu His Leu Ile Ser Leu Val  
 35 40 45  
 Gly Ser Leu Leu Glu Arg Arg Ser Cys Arg Asp Pro Trp Trp Arg Gly  
 50 55 60  
 Gly Lys Lys Met Ser Gly Ala Ala Leu Val Ala Ile Ala Ala Ser Ile  
 65 70 75 80  
 Gly Asn Leu Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val  
 85 90 95  
 Leu Tyr Ile Lys Lys Glu Phe Gln Leu Glu Asn Asn Pro Thr Val Glu  
 100 105 110  
 Gly Leu Ile Val Ala  
 115

<210> 13  
 <211> 1487  
 <212> DNA  
 <213> Triticum aestivum

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 gaatctacttgcaccaagagggggtggccgactcaagaaggggctctgtgttttcaacttc180  
 ctggtgggggtgatgccacgcaaggggggcatggtgtttatcatgctgctgcttttggttaa240  
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 gtgtgaggcgtgcattgttcgtcgggtgttgaattcagatgcttcagcagtttgctggaa420  
 taaatggagtctctacttatctcctcaaa ttctggagcagctgggtgtgctgtttcttc480  
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 tactcatgctccaagcattggtgtagccatgagacttatggatatatctggaagaagggt600  
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 ttggtatata tgcagtcgttgctgcatctctttgtgttcgtctacctaaaggtcccag960  
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10051909 Sequence Listing.txt

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cgcaggccac cattgcctga ttcatcatgg agctttgttt tcagtttgca cactgcggtc 1080
tgcgctgaaa attgcaaatt ggacgggtcc tcgtgaggaa cggaaaaact tttgagttgt 1140
aaatgagaca gctacccaaa gagctcatca cgaggaacgg gaagctgtaa aagtaggagg 1200
atctcatgcc cccatttcac cgtctattat tgcttattag tactgtactg taatcgtcac 1260
tagttgctgt agggttgttc aacttgctaa tctgattctg aactaccatg ctgatgtccg 1320
aaataaagaa aaagcatgtt tttttttgtg tcaacttgca aactttcttt taaacattgt 1380
gcaatgtatt gtaaatttct ttatcaactt ccctcgattc agagagaagc acttgtttgt 1440
aagtcatgaa agatttttct cgacaaaaaa aaaaaaaaaa aaaaaaaa 1487

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 <211> 345  
 <212> PRT  
 <213> Triticum aestivum

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 Gly Trp Gln Leu Ala Trp Lys Trp Ser Glu Arg Gln Gly Glu Asp Gly  
 20 25 30  
 Lys Lys Glu Gly Gly Phe Lys Arg Ile Tyr Leu His Gln Glu Gly Val  
 35 40 45  
 Ala Asp Ser Arg Arg Gly Ser Val Val Ser Leu Pro Gly Gly Gly Asp  
 50 55 60  
 Ala Thr Gln Gly Gly Ser Gly Phe Ile His Ala Ala Ala Leu Val Ser  
 65 70 75 80  
 His Ser Ala Leu Tyr Ser Lys Asp Leu Met Glu Glu Arg Met Ala Ala  
 85 90 95  
 Gly Pro Ala Met Ile His Pro Leu Glu Ala Ala Pro Lys Gly Ser Ile  
 100 105 110  
 Trp Lys Asp Leu Phe Glu Pro Gly Val Arg Arg Ala Leu Phe Val Gly  
 115 120 125  
 Val Gly Ile Gln Met Leu Gln Gln Phe Ala Gly Ile Asn Gly Val Leu  
 130 135 140  
 Tyr Tyr Thr Pro Gln Ile Leu Glu Gln Ala Gly Val Ala Val Leu Leu  
 145 150 155 160  
 Ser Asn Leu Gly Leu Ser Ser Ala Ser Ala Ser Ile Leu Ile Ser Ser  
 165 170 175  
 Leu Thr Thr Leu Leu Met Leu Pro Ser Ile Gly Val Ala Met Arg Leu  
 180 185 190  
 Met Asp Ile Ser Gly Arg Arg Phe Leu Leu Leu Gly Thr Ile Pro Ile  
 195 200 205  
 Leu Ile Ala Ser Leu Ile Val Leu Gly Val Val Asn Val Ile Asn Leu  
 210 215 220  
 Ser Thr Val Pro His Ala Val Leu Ser Thr Val Ser Val Ile Val Tyr  
 225 230 235 240  
 Phe Cys Cys Phe Val Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys  
 245 250 255

10051909 Sequence Listing.txt

Ala Glu Ile Phe Pro Thr Arg Val Arg Gly Val Cys Ile Ala Ile Cys  
260 265 270

Ala Leu Thr Phe Trp Ile Cys Asp Ile Ile Val Thr Tyr Ser Leu Pro  
275 280 285

Val Met Leu Asn Ala Ile Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala  
290 295 300

Val Val Cys Cys Ile Ala Phe Val Phe Val Tyr Leu Lys Val Pro Glu  
305 310 315 320

Thr Lys Gly Met Pro Leu Glu Val Ile Thr Glu Phe Phe Ala Val Gly  
325 330 335

Ala Lys Gln Ala Gln Ala Thr Ile Ala  
340 345

<210> 15  
<211> 1009  
<212> DNA  
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aagaagggtt cttctccttt caacaatccc tgtcttgata gtagcgctag ctgtcttggt 300  
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aaagcagggc aaggaagcca cggactagtt gctctgatcc ggtgatccgc gtcgctggtg 720  
gtaattttgt ggtgtcataa ctactactac actggttaac ctgcatgct ttggtgaaga 780  
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tcgattatgt gtttgcctaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1009

<210> 16  
<211> 228  
<212> PRT  
<213> Triticum aestivum

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20 25 30

Ile Leu Glu Gln Ala Gly Val Gly Val Leu Leu Ser Asn Ile Gly Leu  
35 40 45

Ser Ser Ser Ser Ala Ser Ile Leu Ile Ser Ala Leu Thr Thr Leu Leu  
50 55 60

Met Leu Pro Ser Ile Gly Ile Ala Met Arg Leu Met Asp Met Ser Gly  
65 70 75 80

10051909 Sequence Listing.txt

Arg Arg Phe Leu Leu Leu Ser Thr Ile Pro Val Leu Ile Val Ala Leu  
85 90 95  
Ala Val Leu Val Leu Val Asn Val Leu Asp Val Gly Thr Met Val His  
100 105 110  
Ala Ala Leu Ser Thr Ile Ser Val Ile Val Tyr Phe Cys Phe Phe Val  
115 120 125  
Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe Pro  
130 135 140  
Thr Ser Val Arg Gly Ile Cys Ile Ala Ile Cys Ala Leu Thr Phe Trp  
145 150 155 160  
Ile Gly Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn Ala  
165 170 175  
Ile Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Ile Val Cys Val Leu  
180 185 190  
Ala Phe Val Phe Val Tyr Met Lys Val Pro Glu Thr Lys Gly Met Pro  
195 200 205  
Leu Glu Val Ile Thr Glu Phe Phe Ser Val Gly Ala Lys Gln Gly Lys  
210 215 220

Glu Ala Thr Asp  
225

<210> 17  
<211> 615  
<212> DNA  
<213> Zea mays

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<220>  
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<222> (476)

10051909 Sequence Listing.txt

<223> n = a, c, g or t

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<222> (599)

<223> n = a, c, g or t

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<222> (602)

<223> n = a, c, g or t

<400> 17

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aggcaacgtc	aagttcgctt	tcgcctgcnc	catcctcgcc	tcaatgacct	ccatccttct	180
cggctatgat	atcggagtga	tgagcggcgc	gtcgttgtag	atcaagaagg	acctgaaaat	240
cagcgacgtg	aagctggaga	tcctgatggg	natcctcaac	gtgtactcgc	tcacggctc	300
gttngcggca	gggcggacgt	ccgactggat	cggncgccgt	acaccatcgt	gttcgcngcg	360
gtgatcttct	tcgcgggcgc	ttcctcatgg	gcttcgccgt	gaactactgg	atgctcatgt	420
tcgggcgctt	cgtggccggg	atcggcgtgg	gctacgcgct	catgatcgca	accgtntaca	480
cggccgaagt	gtccccgcat	cggcccgcgg	cttcctgacg	tcgttcccgg	aggtgttcat	540
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cnctaagtgc	ggcat					615

<210> 18

<211> 167

<212> PRT

<213> Zea mays

<220>

<221> UNSURE

<222> (34)

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<220>

<221> UNSURE

<222> (85)

<223> Xaa = any amino acid

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<221> UNSURE

<222> (98)

<223> Xaa = any amino acid

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<222> (151)

<223> Xaa = any amino acid

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Ala	Ala	Ile	Glu	Pro	Gly	Lys	Lys	Gly	Asn	Val	Lys	Phe	Ala	Phe	Ala
			20					25					30		

Cys	Xaa	Ile	Leu	Ala	Ser	Met	Thr	Ser	Ile	Leu	Leu	Gly	Tyr	Asp	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## 10051909 Sequence Listing.txt

35

40

45

Gly Val Met Ser Gly Ala Ser Leu Tyr Ile Lys Lys Asp Leu Lys Ile  
 50 55 60  
 Ser Asp Val Lys Leu Glu Ile Leu Met Gly Ile Leu Asn Val Tyr Ser  
 65 70 75 80  
 Leu Ile Gly Ser Xaa Ala Ala Gly Arg Thr Ser Asp Trp Ile Gly Arg  
 85 90 95  
 Arg Xaa Thr Ile Val Phe Ala Ala Val Ile Phe Phe Ala Gly Ala Xaa  
 100 105 110  
 Leu Met Gly Phe Ala Val Asn Tyr Trp Met Leu Met Phe Gly Arg Phe  
 115 120 125  
 Val Ala Gly Ile Gly Val Gly Tyr Ala Leu Met Ile Ala Thr Val Tyr  
 130 135 140  
 Thr Ala Glu Val Ser Pro Xaa Ser Ala Arg Gly Phe Leu Thr Ser Phe  
 145 150 155 160  
 Pro Glu Val Phe Ile Thr Ser  
 165

<210> 19  
 <211> 1914  
 <212> DNA  
 <213> Zea mays

<400> 19  
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 catatgtgcc atcctggcct ccatggcctc tgtcatcctt ggctatgaca ttgggggtgat 180  
 gagtggagcg gccatgtaca tcaagaagga cctgaatatc acggacgtgc agctggagat 240  
 cctgatcggg atcctcagtc tctactcgct gttcggatcc ttcgctggcg cgcggacgtc 300  
 cgacaggatc gggcgccgct tgaccgtcgt gttcgccgct gtcattcttct tcgtgggctc 360  
 gttgctcatg ggtttcgccg tcaactacgg catgctcatg gcggggccgct tcgtggccgg 420  
 agtcggtgtg ggctacgggg gcatgatcgc gcccggtgtac acggccgaga tctcgcctgc 480  
 ggcgtcccgt ggcttcctga ccaccttccc ggaggtgttc atcaacatcg gcatcctgct 540  
 tggctacctg tccaacttcg cgttcgcgcg cctcccgtc cacctcggct ggcgcgtcat 600  
 gctcgccatt ggcgagttc cgtccggcct gctcgcgctc ctggtgttct gcatgcccga 660  
 gtcgcctcgg tggctgggtc tgaagggccg cctcgcggac gccagggctg tgctagagaa 720  
 gacctctgcc acgccagagg aggccgccga gcggctggcc gacatcaagg ccgcggcggg 780  
 gattccgaag ggctcgcag gggacgtagt caccgtaccc ggcaaggagc aaggcggcgg 840  
 tgagttgcag gtgtggaaga agctcatcct gtccccgacc ccggtgttcc gacgcatact 900  
 gctctcggcc gtgggtctcc acttcttcca gcaggcttct ggcaagcact ccgtcgtcca 960  
 gtacagcgcc cgcctgttca agagcgcggg gatcaccgac gacaacaagc tcctgggctg 1020  
 cacctgcgcg gtgggcgtga ccaagacgtt cttcatcctg gtggccacgt tcctgctgga 1080  
 ccgcgcgggg cgtcggcctc tgctgctgat cagcacgggc gggatgattg tctcgtcat 1140  
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 cgtcgccctg tgcatcgcgt caaccctgtc ctacatcgcc ttcttctcca tcggcctcgg 1260  
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 cgcttggtt ttcttcttca cgtgcctccc ggagacacgc ggccggacgc tggaggagat 1500  
 gggcaagctg ttcggcatgc cagacacggg catggctgaa gaagcagaag acgccgcagc 1560  
 caaggagaag gtggtggaac tgcctagcag caagtaggtg gctatcccag agcacaggctc 1620  
 aagtgaagta gatggacaag atcattgtct tttcaactaa ttagatgggc aagaataact 1680  
 aagactgccc tatgaggtgt cgtggttcaa ccagagatca ttctgctcct tttcttttcc 1740  
 cttccttttt cgagtaccat tcccattcgt cgtggtcagt acgatgttgg gtcgttggga 1800  
 gttagtgggtg tcagagtccg cgtgtgcttt gcaagccagg gctgaacca caatcatcag 1860

## 10051909 Sequence Listing.txt

1914

taacaaaaat tcttccgttt gctttgcaag ccaaaaaaaaaa aaaaaaaaaa aaaa

<210> 20  
 <211> 513  
 <212> PRT  
 <213> Zea mays

<400> 20  
 Met Ala Ser Asp Glu Leu Ala Lys Ala Val Glu Pro Arg Lys Lys Gly  
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 Asn Val Lys Tyr Ala Ser Ile Cys Ala Ile Leu Ala Ser Met Ala Ser  
 20 25 30  
 Val Ile Leu Gly Tyr Asp Ile Gly Val Met Ser Gly Ala Ala Met Tyr  
 35 40 45  
 Ile Lys Lys Asp Leu Asn Ile Thr Asp Val Gln Leu Glu Ile Leu Ile  
 50 55 60  
 Gly Ile Leu Ser Leu Tyr Ser Leu Phe Gly Ser Phe Ala Gly Ala Arg  
 65 70 75 80  
 Thr Ser Asp Arg Ile Gly Arg Arg Leu Thr Val Val Phe Ala Ala Val  
 85 90 95  
 Ile Phe Phe Val Gly Ser Leu Leu Met Gly Phe Ala Val Asn Tyr Gly  
 100 105 110  
 Met Leu Met Ala Gly Arg Phe Val Ala Gly Val Gly Val Gly Tyr Gly  
 115 120 125  
 Gly Met Ile Ala Pro Val Tyr Thr Ala Glu Ile Ser Pro Ala Ala Ser  
 130 135 140  
 Arg Gly Phe Leu Thr Thr Phe Pro Glu Val Phe Ile Asn Ile Gly Ile  
 145 150 155 160  
 Leu Leu Gly Tyr Leu Ser Asn Phe Ala Phe Ala Arg Leu Pro Leu His  
 165 170 175  
 Leu Gly Trp Arg Val Met Leu Ala Ile Gly Ala Val Pro Ser Gly Leu  
 180 185 190  
 Leu Ala Leu Leu Val Phe Cys Met Pro Glu Ser Pro Arg Trp Leu Val  
 195 200 205  
 Leu Lys Gly Arg Leu Ala Asp Ala Arg Ala Val Leu Glu Lys Thr Ser  
 210 215 220  
 Ala Thr Pro Glu Glu Ala Ala Glu Arg Leu Ala Asp Ile Lys Ala Ala  
 225 230 235 240  
 Ala Gly Ile Pro Lys Gly Leu Asp Gly Asp Val Val Thr Val Pro Gly  
 245 250 255  
 Lys Glu Gln Gly Gly Gly Glu Leu Gln Val Trp Lys Lys Leu Ile Leu  
 260 265 270  
 Ser Pro Thr Pro Ala Val Arg Arg Ile Leu Leu Ser Ala Val Gly Leu  
 275 280 285  
 His Phe Phe Gln Gln Ala Ser Gly Ser Asp Ser Val Val Gln Tyr Ser

10051909 Sequence Listing.txt

290	295	300
Ala Arg Leu Phe Lys Ser	Ala Gly Ile Thr Asp Asp Asn Lys Leu Leu	
305	310	315
Gly Val Thr Cys Ala Val Gly Val Thr Lys Thr Phe Phe Ile Leu Val		
	325	330
Ala Thr Phe Leu Leu Asp Arg Ala Gly Arg Arg Pro Leu Leu Leu Ile		
	340	345
Ser Thr Gly Gly Met Ile Val Ser Leu Ile Cys Leu Gly Ser Gly Leu		
	355	360
Thr Val Ala Gly His His Pro Asp Thr Lys Val Ala Trp Ala Val Ala		
	370	375
Leu Cys Ile Ala Ser Thr Leu Ser Tyr Ile Ala Phe Phe Ser Ile Gly		
	385	390
Leu Gly Pro Ile Thr Gly Val Tyr Thr Ser Glu Ile Phe Pro Leu Gln		
	405	410
Val Arg Ala Leu Gly Phe Ala Val Gly Val Ala Ser Asn Arg Val Thr		
	420	425
Ser Ala Val Ile Ser Met Thr Phe Leu Ser Leu Ser Lys Ala Ile Thr		
	435	440
Ile Gly Gly Ser Phe Phe Leu Tyr Ser Gly Ile Ala Ala Val Ala Trp		
	450	455
Val Phe Phe Phe Thr Cys Leu Pro Glu Thr Arg Gly Arg Thr Leu Glu		
	465	470
Glu Met Gly Lys Leu Phe Gly Met Pro Asp Thr Gly Met Ala Glu Glu		
	485	490
Ala Glu Asp Ala Ala Ala Lys Glu Lys Val Val Glu Leu Pro Ser Ser		
	500	505
		510

Lys

<210> 21  
 <211> 2017  
 <212> DNA  
 <213> Oryza sativa

<400>	21					
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ccgtcgcgcc	gaagaagaag	ggcaacgtcc	ggttcgcctt	cgcctgcgcc	atcctcgcct	180
ccatgacctc	catcctcctc	ggctacgata	tcgggggtgat	gagcggggcg	tcgctgtaca	240
tcaagaagga	cttcaacatc	agtgacggga	aggtggaggt	tctcatgggc	atactgaacc	300
tctactcgct	catcggctcc	ttcgcggcgg	ggcggacgtc	ggactggatc	ggccggcggt	360
acaccatcgt	gttcgccgcc	gtcatattct	tcgcgggggs	gttcctcatg	gggttcgccg	420
tcaactacgc	catgctcatg	ttcggccgct	tcgtggcccg	catcggcgtg	ggctacgcgc	480
tcatgatcgc	gccggtgtac	accgccgagg	tgtcggccgc	gtcggcgcgt	ggcttcctga	540
cgtcgttccc	ggaggtgttc	atcaacttcg	gcatcctgct	cgggtacgtc	tcgaactatg	600
ctttctcccg	cttgccgctg	aacctcgggt	ggcgcacatc	gctcggcatc	ggcgcggcgc	660
cgtccgtgct	gctcgcgctc	atggtgctcg	gcatgccgga	gtcggccgcg	tggctggtca	720
tgaagggacg	cctcgcggac	gccaaaggtgg	tgctggagaa	gacctccgac	acggcggagg	780

10051909 Sequence Listing.txt

```

aggccgcgga ggcgcctggcc gacatcaagg ccgccgccgg catccctgag gagctcgacg 840
gcgacgtggt gaccgtcccc aagagagggg gcggaaacga gaagcgggtg tggaaggagc 900
tcatcctgtc cccgaccccg gccatgcggc gcatcctgct gtccgggatc ggcattccact 960
tcttccagca tgcgttgggc attcactccg tcgtcttcta cagccctctc gtgttcaaga 1020
gccccggatt aacgaacgac aaacacttct tgggcaccac ttggccgttc ggtgtcacca 1080
agaggctttt catcttggtg gcgactttct tcatcgacgg cgtcgggcgg cggccgctgt 1140
tgctgggcag cacgggcggg ataatcctct ccctcatcgg cctcggcgcc gggctcaccg 1200
tcgtcggcca gcaccccgac gccaagatac cttgggccat cggcctaagc atcgcctcca 1260
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acctcccgga gacccgcggc cggacgctgg aggagatgag caagctgttc ggcgacacgg 1560
ccgccgcctc ggaatcagac gagccagcca aggagaagaa gaaggtggaa atggccgcca 1620
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tgctgtactg gctagctagc aagtagtagc agcaacgtgg gaagattcgc tgatccggcg 1740
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tcatcttcaa gtacatggat tttattttgc tctttgcttt gtccgtaaaa gttgtactat 1860
gcgatgaaga ataccagtat gtagcaaggc tgaggttgtg tgtagctact agaagtgtca 1920
gtcacgttgt tcttgtaaga aatgtttaac tgtaatttaa gcagtattgt tgcagtaatc 1980
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 2017

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<210> 22  
 <211> 510  
 <212> PRT  
 <213> Oryza sativa

<220>  
 <221> UNSURE  
 <222> (102)  
 <223> Xaa = any amino acid

<400> 22  
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 Asn Val Arg Phe Ala Phe Ala Cys Ala Ile Leu Ala Ser Met Thr Ser  
 20 25 30  
 Ile Leu Leu Gly Tyr Asp Ile Gly Val Met Ser Gly Ala Ser Leu Tyr  
 35 40 45  
 Ile Lys Lys Asp Phe Asn Ile Ser Asp Gly Lys Val Glu Val Leu Met  
 50 55 60  
 Gly Ile Leu Asn Leu Tyr Ser Leu Ile Gly Ser Phe Ala Ala Gly Arg  
 65 70 75 80  
 Thr Ser Asp Trp Ile Gly Arg Arg Tyr Thr Ile Val Phe Ala Ala Val  
 85 90 95  
 Ile Phe Phe Ala Gly Xaa Phe Leu Met Gly Phe Ala Val Asn Tyr Ala  
 100 105 110  
 Met Leu Met Phe Gly Arg Phe Val Ala Gly Ile Gly Val Gly Tyr Ala  
 115 120 125  
 Leu Met Ile Ala Pro Val Tyr Thr Ala Glu Val Ser Pro Ala Ser Ala  
 130 135 140  
 Arg Gly Phe Leu Thr Ser Phe Pro Glu Val Phe Ile Asn Phe Gly Ile  
 145 150 155 160

10051909 Sequence Listing.txt

Leu Leu Gly Tyr Val Ser Asn Tyr Ala Phe Ser Arg Leu Pro Leu Asn  
 165 170 175  
 Leu Gly Trp Arg Ile Met Leu Gly Ile Gly Ala Ala Pro Ser Val Leu  
 180 185 190  
 Leu Ala Leu Met Val Leu Gly Met Pro Glu Ser Pro Arg Trp Leu Val  
 195 200 205  
 Met Lys Gly Arg Leu Ala Asp Ala Lys Val Val Leu Glu Lys Thr Ser  
 210 215 220  
 Asp Thr Ala Glu Glu Ala Ala Glu Arg Leu Ala Asp Ile Lys Ala Ala  
 225 230 235 240  
 Ala Gly Ile Pro Glu Glu Leu Asp Gly Asp Val Val Thr Val Pro Lys  
 245 250 255  
 Arg Gly Ser Gly Asn Glu Lys Arg Val Trp Lys Glu Leu Ile Leu Ser  
 260 265 270  
 Pro Thr Pro Ala Met Arg Arg Ile Leu Leu Ser Gly Ile Gly Ile His  
 275 280 285  
 Phe Phe Gln His Ala Leu Gly Ile His Ser Val Val Phe Tyr Ser Pro  
 290 295 300  
 Leu Val Phe Lys Ser Pro Gly Leu Thr Asn Asp Lys His Phe Leu Gly  
 305 310 315 320  
 Thr Thr Trp Pro Phe Gly Val Thr Lys Arg Leu Phe Ile Leu Leu Ala  
 325 330 335  
 Thr Phe Phe Ile Asp Gly Val Gly Arg Arg Pro Leu Leu Leu Gly Ser  
 340 345 350  
 Thr Gly Gly Ile Ile Leu Ser Leu Ile Gly Leu Gly Ala Gly Leu Thr  
 355 360 365  
 Val Val Gly Gln His Pro Asp Ala Lys Ile Pro Trp Ala Ile Gly Leu  
 370 375 380  
 Ser Ile Ala Ser Thr Leu Ala Tyr Val Ala Phe Phe Ser Ile Gly Leu  
 385 390 395 400  
 Gly Pro Ile Thr Trp Val Tyr Ser Ser Glu Ile Phe Pro Leu Gln Val  
 405 410 415  
 Arg Ala Leu Gly Cys Ser Leu Gly Val Ala Ala Asn Arg Val Thr Ser  
 420 425 430  
 Gly Val Ile Ser Met Thr Phe Leu Ser Leu Ser Lys Ala Ile Thr Ile  
 435 440 445  
 Gly Gly Ser Phe Phe Leu Tyr Ser Gly Ile Ala Ala Leu Ala Trp Val  
 450 455 460  
 Phe Phe Tyr Thr Tyr Leu Pro Glu Thr Arg Gly Arg Thr Leu Glu Glu  
 465 470 475 480  
 Met Ser Lys Leu Phe Gly Asp Thr Ala Ala Ala Ser Glu Ser Asp Glu  
 485 490 495

10051909 Sequence Listing.txt

Pro Ala Lys Glu Lys Lys Lys Val Glu Met Ala Ala Thr Asn  
500 505 510

<210> 23  
<211> 1853  
<212> DNA  
<213> Glycine max

<400> 23  
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aattaaatta aatacatgct agcactttaaa cagtactcct ttctctaata tcttctctcat 120  
atttttccttt ctgcgatat ttagctaat aaactaagtc actaagatga ctgagggaaa 180  
gctagttaga gctgcagaag ctcataagac acttcaggat ttcgatactc caaagaagcg 240  
caaaaggaac aagtatgctt ttgcttgtgc tatgctggcc tccatgactt ccatcttgct 300  
tggttatgat attggagtga tgagtggagc agccatatac ataaaaaggg acctgaaagt 360  
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atgtctcgcc ggcagaacct ccgactggat aggtccccgt tacacgattg ttttcgccgg 480  
caccatcttc tttgtcggag cacttctcat gggtttctcc cccaattatt ctttctcat 540  
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caccgccgag gtctccccgg cctcctctcg tggcttcctc acttccttcc ctgaggtatt 660  
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aggagtgttg gcgatgccgg agtccccaaag gtggcttgtg atgaggggtc gtttgggaga 840  
ggcaagaaaa gtgcttaaca aaacctcaga cagcaaggaa gaggcccaac taaggctagc 900  
ggaaatcaaa caagccgcag ggatccccga gagttgcaac gacgacgtcg ttcaggtaaa 960  
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cgccgctcgt ttgtacagcc ccaggatctt cgaaaaggct gggattacaa acgacacgca 1140  
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gtttacgttg gaccgcgtgg gtcgtcgtcc gttgttattg tctagtgtcg gcggcatggt 1260  
gctctcgctt ctcacgcttg cgatcagcct cactgttatt gatcattcgg agaggaaatt 1320  
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cgaagacatg gaagggtctt ttggtacttt taggtccaaa tccaacgcca gcaaggctgt 1680  
agaaaatgag aatgggcaag tagcacaagt ccagctagga accaatgtcc aaacttgaaa 1740  
aatgagtatt gggacatcca gtaatagtga agtaatttcg tgattttttt tttgtttttt 1800  
acttttttaga ctagttcttc aaatcaaaac gagaagttaa agtgaaaaaa aaa 1853

<210> 24  
<211> 523  
<212> PRT  
<213> Glycine max

<400> 24  
Met Thr Glu Gly Lys Leu Val Glu Ala Ala Glu Ala His Lys Thr Leu  
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20 25 30  
Ala Cys Ala Met Leu Ala Ser Met Thr Ser Ile Leu Leu Gly Tyr Asp  
35 40 45  
Ile Gly Val Met Ser Gly Ala Ala Ile Tyr Ile Lys Arg Asp Leu Lys  
50 55 60  
Val Ser Asp Glu Gln Ile Glu Ile Leu Leu Gly Ile Ile Asn Leu Tyr  
65 70 75 80  
Ser Leu Ile Gly Ser Cys Leu Ala Gly Arg Thr Ser Asp Trp Ile Gly

10051909 Sequence Listing.txt

85

90

95

Pro Arg Tyr Thr Ile Val Phe Ala Gly Thr Ile Phe Phe Val Gly Ala  
100 105 110  
Leu Leu Met Gly Phe Ser Pro Asn Tyr Ser Phe Leu Met Phe Gly Arg  
115 120 125  
Phe Val Ala Gly Ile Gly Ile Gly Tyr Ala Leu Met Ile Ala Pro Val  
130 135 140  
Tyr Thr Ala Glu Val Ser Pro Ala Ser Ser Arg Gly Phe Leu Thr Ser  
145 150 155 160  
Phe Pro Glu Val Phe Ile Asn Gly Gly Ile Leu Ile Gly Tyr Ile Ser  
165 170 175  
Asn Tyr Ala Phe Ser Lys Leu Thr Leu Lys Val Gly Trp Arg Met Met  
180 185 190  
Leu Gly Val Gly Ala Ile Pro Ser Val Leu Leu Thr Val Gly Val Leu  
195 200 205  
Ala Met Pro Glu Ser Pro Arg Trp Leu Val Met Arg Gly Arg Leu Gly  
210 215 220  
Glu Ala Arg Lys Val Leu Asn Lys Thr Ser Asp Ser Lys Glu Glu Ala  
225 230 235 240  
Gln Leu Arg Leu Ala Glu Ile Lys Gln Ala Ala Gly Ile Pro Glu Ser  
245 250 255  
Cys Asn Asp Asp Val Val Gln Val Asn Lys Gln Ser Asn Gly Glu Gly  
260 265 270  
Val Trp Lys Glu Leu Phe Leu Tyr Pro Thr Pro Ala Ile Arg His Ile  
275 280 285  
Val Ile Ala Ala Leu Gly Ile His Phe Phe Gln Gln Ala Ser Gly Val  
290 295 300  
Asp Ala Val Val Leu Tyr Ser Pro Arg Ile Phe Glu Lys Ala Gly Ile  
305 310 315 320  
Thr Asn Asp Thr His Lys Leu Leu Ala Thr Val Ala Val Gly Phe Val  
325 330 335  
Lys Thr Val Phe Ile Leu Ala Ala Thr Phe Thr Leu Asp Arg Val Gly  
340 345 350  
Arg Arg Pro Leu Leu Leu Ser Ser Val Gly Gly Met Val Leu Ser Leu  
355 360 365  
Leu Thr Leu Ala Ile Ser Leu Thr Val Ile Asp His Ser Glu Arg Lys  
370 375 380  
Leu Met Trp Ala Val Gly Ser Ser Ile Ala Met Val Leu Ala Tyr Val  
385 390 395 400  
Ala Thr Phe Ser Ile Gly Ala Gly Pro Ile Thr Trp Val Tyr Ser Ser  
405 410 415  
Glu Ile Phe Pro Leu Arg Leu Arg Ala Gln Gly Ala Ala Ala Gly Val

10051909 Sequence Listing.txt

420

425

430

Ala Val Asn Arg Thr Thr Ser Ala Val Val Ser Met Thr Phe Leu Ser  
435 440 445

Leu Thr Arg Ala Ile Thr Ile Gly Gly Ala Phe Phe Leu Tyr Cys Gly  
450 455 460

Ile Ala Thr Val Gly Trp Ile Phe Phe Tyr Thr Val Leu Pro Glu Thr  
465 470 475 480

Arg Gly Lys Thr Leu Glu Asp Met Glu Gly Ser Phe Gly Thr Phe Arg  
485 490 495

Ser Lys Ser Asn Ala Ser Lys Ala Val Glu Asn Glu Asn Gly Gln Val  
500 505 510

Ala Gln Val Gln Leu Gly Thr Asn Val Gln Thr  
515 520

<210> 25  
<211> 2089  
<212> DNA  
<213> Triticum aestivum

<400> 25

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cggctacgac	atcggcgtga	tgagcggagc	gtcgcgtgtac	atccagaagg	atctgaagat	240
caacgacacc	cagctggagg	tcctcatggg	catcctcaac	gtgtactcgc	tcattggctc	300
cttcgcggcg	ggcgggacgt	ccgactggat	cggccggcgc	ttcaccatcg	tcttcgccgc	360
cgatcatctt	ttcgcggggc	ccctcatcat	gggcttctcc	gtcaactacg	ccatgctcat	420
gttcggggcg	ttcgtggccg	gcatcggcgt	ggggtagcgt	ctcatgatcg	cgcccgtgaa	480
cacgggcgag	gtgtcccccg	cgtctgcccc	tgggggttct	acatccttcc	cggagggtgt	540
catcaacttc	ggcatcctcc	tcggatatgt	ctccaaacttc	gccttcgccc	gcctctccct	600
ccgcctcggc	tggcgcatga	tgctcggcat	aggcgcggtg	ccgtccgtcc	tgctcgcggt	660
catggtgctc	ggcatgcccc	agtctccccg	gtggctcgtc	atgaagggcc	gtctcgcgga	720
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catagccatg	cgccacatcc	tcatcgcggg	aatcggcatc	cacttcttcc	agcagtcttc	960
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cgacagccgt	ctccgcggca	ccaccgtggc	ggtcggggcc	accaatacgg	tcttcatcct	1080
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ggacgagaag	atcacctggg	ccatcgtcct	gtgcatcttc	tgcatcatgg	cctacgtggc	1260
cttcttctcc	atcggcctcg	gccccatcac	gtgggtgtac	agctcggaga	tcttcccgct	1320
gcacgtgcgc	gcgctgggct	gctccctggg	cgtggccgtc	aaccgcctga	ccagcggcgt	1380
gatctccatg	accttcattt	cgtgtgctca	ggccatgacc	atcggcgggc	ccttcttcct	1440
cttcgccggc	atcgccctcat	tcgcatgggt	gttcttcttc	gcctacctgc	cggagaccgc	1500
cggccgcacg	ctggaggaca	tgagctcgct	gttcggcaac	acggccacgc	acaagcaggg	1560
cgccgcggaa	gccgacgacg	acgccgggga	gaagaagggt	gaaatggccg	ccaccaactg	1620
accgcaagtt	ggcagatcgc	gatgcgaaga	cttgcgctgt	atccgtctcg	gctagctagc	1680
tgccacaagg	ccacatagat	gacgaagtag	cgtgggaaga	ttcgtgatc	cggccggagc	1740
tgccggaggg	cgacggcaag	ctccagctcg	atcgagacgt	taatggcttc	ttaaatgtgc	1800
taagtttaat	gtttcgctct	ttggttttgt	ccgggtaggt	cgtgagcaat	ccggtagtgc	1860
cgatgccaa	gctaatacgac	gccggacgga	ctagactact	gtagtagact	gtagagggtg	1920
accgttgcta	cttccgtggc	gtttgtctgc	atgattagga	gagaaaactg	gcggtggttc	1980
gaggactcta	cctgccgatc	gagtgaagtca	agcgagccac	ggaaaatgtg	taagaaaaaa	2040
atattaagta	tgtgtattgt	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		2089

<210> 26

10051909 Sequence Listing.txt

<211> 539  
<212> PRT  
<213> Triticum aestivum

<400> 26  
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Ala Ala Ser Arg Gly Ala Ser Ser Thr Met Asp Arg Ala Ala Leu Pro  
20 25 30  
Ala Ala Val Glu Pro Lys Lys Lys Gly Asn Val Arg Phe Ala Phe Ala  
35 40 45  
Cys Ala Ile Leu Ala Ser Met Thr Ser Ile Leu Leu Gly Tyr Asp Ile  
50 55 60  
Gly Val Met Ser Gly Ala Ser Leu Tyr Ile Gln Lys Asp Leu Lys Ile  
65 70 75 80  
Asn Asp Thr Gln Leu Glu Val Leu Met Gly Ile Leu Asn Val Tyr Ser  
85 90 95  
Leu Ile Gly Ser Phe Ala Ala Gly Arg Thr Ser Asp Trp Ile Gly Arg  
100 105 110  
Arg Phe Thr Ile Val Phe Ala Ala Val Ile Phe Phe Ala Gly Ala Leu  
115 120 125  
Ile Met Gly Phe Ser Val Asn Tyr Ala Met Leu Met Phe Gly Arg Phe  
130 135 140  
Val Ala Gly Ile Gly Val Gly Tyr Ala Leu Met Ile Ala Pro Val Asn  
145 150 155 160  
Thr Gly Glu Val Ser Pro Ala Ser Ala Arg Gly Val Leu Thr Ser Phe  
165 170 175  
Pro Glu Val Phe Ile Asn Phe Gly Ile Leu Leu Gly Tyr Val Ser Asn  
180 185 190  
Phe Ala Phe Ala Arg Leu Ser Leu Arg Leu Gly Trp Arg Ile Met Leu  
195 200 205  
Gly Ile Gly Ala Val Pro Ser Val Leu Leu Ala Phe Met Val Leu Gly  
210 215 220  
Met Pro Glu Ser Pro Arg Trp Leu Val Met Lys Gly Arg Leu Ala Asp  
225 230 235 240  
Ala Lys Val Val Leu Ala Lys Thr Ser Asp Thr Pro Glu Glu Ala Ala  
245 250 255  
Glu Arg Ile Ala Asp Ile Lys Thr Ala Ala Gly Ile Pro Leu Gly Leu  
260 265 270  
Asp Gly Asp Val Val Pro Val Pro Lys Asn Lys Gly Ser Ser Glu Glu  
275 280 285  
Lys Arg Val Leu Lys Asp Leu Ile Leu Ser Pro Thr Ile Ala Met Arg  
290 295 300  
His Ile Leu Ile Ala Gly Ile Gly Ile His Phe Phe Gln Gln Ser Ser

Sequence Listing (text)																		
305						310						315						320
Gly	Ile	Asp	Ala	Val	Val	Leu	Tyr	Ser	Pro	Leu	Val	Phe	Lys	Ser	Ala			
				325					330					335				
Gly	Ile	Thr	Gly	Asp	Ser	Arg	Leu	Arg	Gly	Thr	Thr	Val	Ala	Val	Gly			
			340					345					350					
Ala	Thr	Asn	Thr	Val	Phe	Ile	Leu	Val	Ala	Thr	Phe	Leu	Leu	Asp	Arg			
		355					360					365						
Ile	Arg	Arg	Arg	Pro	Leu	Val	Leu	Thr	Ser	Thr	Gly	Gly	Met	Leu	Val			
	370					375					380							
Ser	Leu	Val	Gly	Leu	Ala	Thr	Gly	Leu	Thr	Val	Ile	Ser	Arg	His	Pro			
385					390					395					400			
Asp	Glu	Lys	Ile	Thr	Trp	Ala	Ile	Val	Leu	Cys	Ile	Phe	Cys	Ile	Met			
				405					410					415				
Ala	Tyr	Val	Ala	Phe	Phe	Ser	Ile	Gly	Leu	Gly	Pro	Ile	Thr	Trp	Val			
			420					425					430					
Tyr	Ser	Ser	Glu	Ile	Phe	Pro	Leu	His	Val	Arg	Ala	Leu	Gly	Cys	Ser			
		435					440					445						
Leu	Gly	Val	Ala	Val	Asn	Arg	Leu	Thr	Ser	Gly	Val	Ile	Ser	Met	Thr			
	450					455					460							
Phe	Ile	Ser	Leu	Ser	Lys	Ala	Met	Thr	Ile	Gly	Gly	Ala	Phe	Phe	Leu			
465					470					475					480			
Phe	Ala	Gly	Ile	Ala	Ser	Phe	Ala	Trp	Val	Phe	Phe	Phe	Ala	Tyr	Leu			
				485					490					495				
Pro	Glu	Thr	Arg	Gly	Arg	Thr	Leu	Glu	Asp	Met	Ser	Ser	Leu	Phe	Gly			
			500					505					510					
Asn	Thr	Ala	Thr	His	Lys	Gln	Gly	Ala	Ala	Glu	Ala	Asp	Asp	Asp	Ala			
		515					520					525						
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	530					535												

<210>	27
<211>	1872
<212>	DNA
<213>	Triticum aestivum

<400>	27						
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ggctttctgct	gcgctcccgg	agccgggggc	agtccatcca	aggaacaagg	gcaatttcaa		180
gtacgccttc	acctgcgccc	tctgtgcttc	catggccacc	atcgtcctcg	gctacgacgt		240
tggggtgatg	agcggtgctg	cgctgtacat	caagagggac	ctgcagatca	cggacgtgca		300
gctggagatc	atgatgggca	tcctgagcgt	gtacgcgctc	atcgggtcct	tcctcggcgc		360
gaggacgtcc	gactgggtcg	gccgccgcgt	caccgtcgct	ttcgcggccg	ccatcttcaa		420
caacggctcc	ttgctcatgg	gcttcgcggt	caactacgcc	atgctcatgg	tcgggcgcctt		480
cgtcaccgga	atcggcgtgg	gctacgccat	catggtcgcg	ccagtgtaca	cgcccgaggt		540
gtccccggcg	tcggcccgcg	gcttcctcac	gtcttttcacc	gaggtgttca	tcaatgtggg		600
catcctcctt	ggctacgtct	ccaactacgc	cttcgcgcgc	ctcccgtcc	acctcagctg		660
gcgcgtcatg	ctcggcatcg	gcgccgtccc	gtccgcacctg	cttgcgctca	tggtgttcgg		720
catgccggag	tctcctcgct	ggctcgtcat	gaaaggccgc	ctcgcggacg	ccagggccgt		780

10051909 Sequence Listing.txt

```

tctggccaag acctccgaca cgccggagga ggccgtggag cgccttgacc agatcaaggc 840
tgccgccggc atccctaggg aacttgacgg cgacgtgggc gtcatgccta agacaaaagg 900
cggccaggag aagcaggtgt ggaaggagct catcttttcg ccgaccccag ccatgcggcg 960
catactgctc gcggcgctcg gcatccattt ctttcagcag gcgacgggct ccgactccgt 1020
cgtgctctat agcccacgcg tgttccagag cgcgggcatc accggcgaca accacctgct 1080
cggcgccaca tgcgccatgg gggtcatgaa gacgctcttc atcctgggtg ccacgttcca 1140
gctcgaccgc gtcggcaggc ggccgctgct gctgaccagc acggccggca tgctcgctg 1200
tctcatcggc ctcgggacgg gcctcaccgt cgtgggctcg caccggacg ccaagggtccc 1260
gtggggccatc ggctgtgca tcgtgtccat cttggcctac gtgtccttct tctccatcgg 1320
cctcggggccc ctcaccagcg tgtacacctc ggaggctctt ccactgcggg tgcgcgcgct 1380
gggcttcgcg ctgggcacgt catgcaaccg cgtcaccagc gccgcgggtc ccatgtcctt 1440
cctgtccttg tccaaggcca tcaccatcgg cggcagcttc ttcctgtacg ccggcatcgc 1500
ggcgatagga tggattttct tcttcacctt cattccggag acgcgtggcc tgccgctcga 1560
ggagataggg aagcttttcg gcatgacgga cacggccgct gaagcccaag acaccgccac 1620
gaaagacaag gcgaaagtag gggagatgaa ctagtgagct agacgtcaac caactgttac 1680
cgatgtacta ccatagagat gtatctgatc aacgtggcaa tataagtgtc acggactctt 1740
ggtgctcatt gatggattgt ttggataaaa tttcaagaga attgtttcaa gtttggatcc 1800
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1860
aaaaaaaaaa aa 1872

```

<210> 28  
 <211> 529  
 <212> PRT  
 <213> Triticum aestivum

<400> 28  
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 Arg Asn Lys Gly Asn Phe Lys Tyr Ala Phe Thr Cys Ala Leu Cys Ala  
 35 40 45  
 Ser Met Ala Thr Ile Val Leu Gly Tyr Asp Val Gly Val Met Ser Gly  
 50 55 60  
 Ala Ser Leu Tyr Ile Lys Arg Asp Leu Gln Ile Thr Asp Val Gln Leu  
 65 70 75 80  
 Glu Ile Met Met Gly Ile Leu Ser Val Tyr Ala Leu Ile Gly Ser Phe  
 85 90 95  
 Leu Gly Ala Arg Thr Ser Asp Trp Val Gly Arg Arg Val Thr Val Val  
 100 105 110  
 Phe Ala Ala Ala Ile Phe Asn Asn Gly Ser Leu Leu Met Gly Phe Ala  
 115 120 125  
 Val Asn Tyr Ala Met Leu Met Val Gly Arg Phe Val Thr Gly Ile Gly  
 130 135 140  
 Val Gly Tyr Ala Ile Met Val Ala Pro Val Tyr Thr Pro Glu Val Ser  
 145 150 155 160  
 Pro Ala Ser Ala Arg Gly Phe Leu Thr Ser Phe Thr Glu Val Phe Ile  
 165 170 175  
 Asn Val Gly Ile Leu Leu Gly Tyr Val Ser Asn Tyr Ala Phe Ala Arg  
 180 185 190  
 Leu Pro Leu His Leu Ser Trp Arg Val Met Leu Gly Ile Gly Ala Val

10051909 Sequence Listing.txt

195					200					205					
Pro	Ser	Ala	Leu	Leu	Ala	Leu	Met	Val	Phe	Gly	Met	Pro	Glu	Ser	Pro
	210					215					220				
Arg	Trp	Leu	Val	Met	Lys	Gly	Arg	Leu	Ala	Asp	Ala	Arg	Ala	Val	Leu
225					230					235					240
Ala	Lys	Thr	Ser	Asp	Thr	Pro	Glu	Glu	Ala	Val	Glu	Arg	Leu	Asp	Gln
				245					250					255	
Ile	Lys	Ala	Ala	Ala	Gly	Ile	Pro	Arg	Glu	Leu	Asp	Gly	Asp	Val	Val
			260					265					270		
Val	Met	Pro	Lys	Thr	Lys	Gly	Gly	Gln	Glu	Lys	Gln	Val	Trp	Lys	Glu
		275					280					285			
Leu	Ile	Phe	Ser	Pro	Thr	Pro	Ala	Met	Arg	Arg	Ile	Leu	Leu	Ala	Ala
	290					295					300				
Leu	Gly	Ile	His	Phe	Phe	Gln	Gln	Ala	Thr	Gly	Ser	Asp	Ser	Val	Val
305					310					315					320
Leu	Tyr	Ser	Pro	Arg	Val	Phe	Gln	Ser	Ala	Gly	Ile	Thr	Gly	Asp	Asn
				325					330					335	
His	Leu	Leu	Gly	Ala	Thr	Cys	Ala	Met	Gly	Val	Met	Lys	Thr	Leu	Phe
			340					345					350		
Ile	Leu	Val	Ala	Thr	Phe	Gln	Leu	Asp	Arg	Val	Gly	Arg	Arg	Pro	Leu
		355					360					365			
Leu	Leu	Thr	Ser	Thr	Ala	Gly	Met	Leu	Ala	Cys	Leu	Ile	Gly	Leu	Gly
	370					375					380				
Thr	Gly	Leu	Thr	Val	Val	Gly	Arg	His	Pro	Asp	Ala	Lys	Val	Pro	Trp
385					390					395					400
Ala	Ile	Gly	Leu	Cys	Ile	Val	Ser	Ile	Leu	Ala	Tyr	Val	Ser	Phe	Phe
				405					410					415	
Ser	Ile	Gly	Leu	Gly	Pro	Leu	Thr	Ser	Val	Tyr	Thr	Ser	Glu	Val	Phe
			420					425					430		
Pro	Leu	Arg	Val	Arg	Ala	Leu	Gly	Phe	Ala	Leu	Gly	Thr	Ser	Cys	Asn
		435					440					445			
Arg	Val	Thr	Ser	Ala	Ala	Val	Ser	Met	Ser	Phe	Leu	Ser	Leu	Ser	Lys
	450					455					460				
Ala	Ile	Thr	Ile	Gly	Gly	Ser	Phe	Phe	Leu	Tyr	Ala	Gly	Ile	Ala	Ala
465					470					475					480
Ile	Gly	Trp	Ile	Phe	Phe	Phe	Thr	Phe	Ile	Pro	Glu	Thr	Arg	Gly	Leu
				485					490					495	
Pro	Leu	Glu	Glu	Ile	Gly	Lys	Leu	Phe	Gly	Met	Thr	Asp	Thr	Ala	Val
			500					505					510		
Glu	Ala	Gln	Asp	Thr	Ala	Thr	Lys	Asp	Lys	Ala	Lys	Val	Gly	Glu	Met
		515					520					525			

Asn

10051909 Sequence Listing.txt

<210> 29  
 <211> 729  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 29  
 Met Ser Gly Ala Val Leu Val Ala Ile Ala Ala Ala Val Gly Asn Leu  
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 Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val Leu Tyr Ile  
 20 25 30  
 Lys Lys Glu Phe Asn Leu Glu Ser Asn Pro Ser Val Glu Gly Leu Ile  
 35 40 45  
 Val Ala Met Ser Leu Ile Gly Ala Thr Leu Ile Thr Thr Cys Ser Gly  
 50 55 60  
 Gly Val Ala Asp Trp Leu Gly Arg Arg Pro Met Leu Ile Leu Ser Ser  
 65 70 75 80  
 Ile Leu Tyr Phe Val Gly Ser Leu Val Met Leu Trp Ser Pro Asn Val  
 85 90 95  
 Tyr Val Leu Leu Leu Gly Arg Leu Leu Asp Gly Phe Gly Val Gly Leu  
 100 105 110  
 Val Val Thr Leu Val Pro Ile Tyr Ile Ser Glu Thr Ala Pro Pro Glu  
 115 120 125  
 Ile Arg Gly Leu Leu Asn Thr Leu Pro Gln Phe Thr Gly Ser Gly Gly  
 130 135 140  
 Met Phe Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Met Pro Ser  
 145 150 155 160  
 Pro Ser Trp Arg Leu Met Leu Gly Val Leu Phe Ile Pro Ser Leu Val  
 165 170 175  
 Phe Phe Phe Leu Thr Val Phe Phe Leu Pro Glu Ser Pro Arg Trp Leu  
 180 185 190  
 Val Ser Lys Gly Arg Met Leu Glu Ala Lys Arg Val Leu Gln Arg Leu  
 195 200 205  
 Arg Gly Arg Glu Asp Val Ser Gly Glu Met Ala Leu Leu Val Glu Gly  
 210 215 220  
 Leu Gly Ile Gly Gly Glu Thr Thr Ile Glu Glu Tyr Ile Ile Gly Pro  
 225 230 235 240  
 Ala Asp Glu Val Thr Asp Asp His Asp Ile Ala Val Asp Lys Asp Gln  
 245 250 255  
 Ile Lys Leu Tyr Gly Ala Glu Glu Gly Leu Ser Trp Val Ala Arg Pro  
 260 265 270  
 Val Lys Gly Gly Ser Thr Met Ser Val Leu Ser Arg His Gly Ser Thr  
 275 280 285  
 Met Ser Arg Arg Gln Gly Ser Leu Ile Asp Pro Leu Val Thr Leu Phe

10051909 Sequence Listing.txt

290	295	300													
Gly 305	Ser	Val	His	Glu	Lys 310	Met	Pro	Asp	Thr	Gly 315	Ser	Met	Arg	Ser	Ala 320
Leu	Phe	Pro	His	Phe 325	Gly	Ser	Met	Phe	Ser 330	Val	Gly	Gly	Asn	Gln 335	Pro
Arg	His	Glu	Asp 340	Trp	Asp	Glu	Glu	Asn 345	Leu	Val	Gly	Glu	Gly 350	Glu	Asp
Tyr	Pro	Ser 355	Asp	His	Gly	Asp	Asp 360	Ser	Glu	Asp	Asp	Leu 365	His	Ser	Pro
Leu	Ile 370	Ser	Arg	Gln	Thr	Thr 375	Ser	Met	Glu	Lys	Asp 380	Met	Pro	His	Thr
Ala 385	His	Gly	Thr	Leu	Ser 390	Thr	Phe	Arg	His	Gly 395	Ser	Gln	Val	Gln	Gly 400
Ala	Gln	Gly	Glu	Gly 405	Ala	Gly	Ser	Met	Gly 410	Ile	Gly	Gly	Gly	Trp 415	Gln
Val	Ala	Trp	Lys 420	Trp	Thr	Glu	Arg	Glu 425	Asp	Glu	Ser	Gly	Gln 430	Lys	Glu
Glu	Gly	Phe 435	Pro	Gly	Ser	Arg	Arg 440	Gly	Ser	Ile	Val	Ser 445	Leu	Pro	Gly
Gly	Asp 450	Gly	Thr	Gly	Glu	Ala 455	Asp	Phe	Val	Gln	Ala 460	Ser	Ala	Leu	Val
Ser 465	Gln	Pro	Ala	Leu	Tyr 470	Ser	Lys	Asp	Leu	Leu 475	Lys	Glu	His	Thr	Ile 480
Gly	Pro	Ala	Met	Val 485	His	Pro	Ser	Glu	Thr 490	Thr	Lys	Gly	Ser	Ile 495	Trp
His	Asp	Leu	His 500	Asp	Pro	Gly	Val	Lys 505	Arg	Ala	Leu	Val	Val 510	Gly	Val
Gly	Leu	Gln 515	Ile	Leu	Gln	Gln	Phe 520	Ser	Gly	Ile	Asn	Gly 525	Val	Leu	Tyr
Tyr	Thr 530	Pro	Gln	Ile	Leu	Glu 535	Gln	Ala	Gly	Val	Gly 540	Ile	Leu	Leu	Ser
Asn 545	Met	Gly	Ile	Ser	Ser 550	Ser	Ser	Ala	Ser	Leu 555	Leu	Ile	Ser	Ala	Leu 560
Thr	Thr	Phe	Val	Met 565	Leu	Pro	Ala	Ile	Ala 570	Val	Ala	Met	Arg	Leu 575	Met
Asp	Leu	Ser	Gly 580	Arg	Arg	Thr	Leu	Leu 585	Leu	Thr	Thr	Ile	Pro 590	Ile	Leu
Ile	Ala	Ser 595	Leu	Leu	Val	Leu	Val 600	Ile	Ser	Asn	Leu	Val 605	His	Met	Asn
Ser	Ile 610	Val	His	Ala	Val	Leu	Ser	Thr	Val	Ser	Val 620	Val	Leu	Tyr	Phe
Cys	Phe	Phe	Val	Met	Gly	Phe	Gly	Pro	Ala	Pro	Asn	Ile	Leu	Cys	Ser

## 10051909 Sequence Listing.txt

Sequence Listing.txt															
625				630				635				640			
Glu	Ile	Phe	Pro	Thr 645	Arg	Val	Arg	Gly	Ile 650	Cys	Ile	Ala	Ile	Cys 655	Ala
Leu	Thr	Phe	Trp 660	Ile	Cys	Asp	Ile	Ile 665	Val	Thr	Tyr	Ser	Leu 670	Pro	Val
Leu	Leu	Lys 675	Ser	Ile	Gly	Leu	Ala 680	Gly	Val	Phe	Gly	Met 685	Tyr	Ala	Ile
Val	Cys 690	Cys	Ile	Ser	Trp	Val 695	Phe	Val	Phe	Ile	Lys 700	Val	Pro	Glu	Thr
Lys 705	Gly	Met	Pro	Leu	Glu 710	Val	Ile	Thr	Glu	Phe 715	Phe	Ser	Val	Gly	Ala 720
Arg	Gln	Ala	Glu	Ala 725	Ala	Lys	Asn	Glu							

<210>	30
<211>	549
<212>	PRT
<213>	Beta vulgaris

<400>	30															
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Ala	Ser	Lys	Val	Ile	Ala	Asp	Phe	Asp	Pro	Leu	Lys	Lys	Pro	Pro	Lys	
			20					25					30			
Arg	Asn	Lys	Phe	Ala	Phe	Ala	Cys	Ala	Thr	Leu	Ala	Ser	Met	Thr	Ser	
		35					40					45				
Val	Leu	Leu	Gly	Tyr	Asp	Ile	Gly	Val	Met	Ser	Gly	Ala	Ile	Ile	Tyr	
	50					55					60					
Leu	Lys	Glu	Asp	Trp	His	Ile	Ser	Asp	Thr	Gln	Ile	Gly	Val	Leu	Val	
65					70					75					80	
Gly	Ile	Leu	Asn	Ile	Tyr	Cys	Leu	Phe	Gly	Ser	Phe	Ala	Ala	Gly	Arg	
				85					90					95		
Thr	Ser	Asp	Trp	Ile	Gly	Arg	Arg	Tyr	Thr	Ile	Val	Leu	Ala	Gly	Ala	
			100					105					110			
Ile	Phe	Phe	Val	Gly	Ala	Leu	Leu	Met	Gly	Phe	Ala	Thr	Asn	Tyr	Ala	
		115					120					125				
Phe	Leu	Met	Val	Gly	Arg	Phe	Val	Thr	Gly	Ile	Gly	Val	Gly	Tyr	Ala	
	130					135					140					
Leu	Met	Ile	Ala	Pro	Val	Tyr	Thr	Ala	Glu	Val	Ser	Pro	Ala	Ser	Ser	
145					150					155					160	
Arg	Gly	Phe	Leu	Thr	Ser	Phe	Pro	Glu	Val	Phe	Ile	Asn	Ala	Gly	Ile	
				165					170					175		
Leu	Leu	Gly	Tyr	Ile	Ser	Asn	Leu	Ala	Phe	Ser	Ser	Leu	Pro	Thr	His	
			180					185					190			
Leu	Ser	Trp	Arg	Phe	Met	Leu	Gly	Ile	Gly	Ala	Ile	Pro	Ser	Ile	Phe	

10051909 Sequence Listing.txt

195		200		205
Leu	Ala	Ile	Gly	Val
210				
Leu	Ala	Met	Pro	Glu
215				
Pro	Arg	Trp	Leu	Val
220				
Met	Gln	Gly	Arg	Leu
225				
Gly	Asp	Ala	Lys	Lys
230				
Val	Leu	Asn	Arg	Ile
235				
Ser	Glu	Ile	Lys	Gln
240				
Thr				
245				
Ala	Gln	Leu	Arg	Leu
250				
Ser	Glu	Ile	Lys	Gln
255				
Thr				
260				
Ala	Glu	Cys	Asp	Glu
265				
Asp	Ile	Tyr	Lys	Val
270				
Glu	Lys			
275				
Thr	Lys	Ile	Lys	Ser
280				
Gly	Asn	Ala	Val	Trp
285				
Lys	Glu	Leu	Phe	Phe
290				
Asn				
295				
Ala	Val	Ile	Ala	Gly
300				
Ile	Gly	Ile	His	
305				
Phe	Phe	Gln	Gln	Ala
310				
Ser	Gly	Ile	Asp	Ala
315				
Val	Val	Leu	Tyr	Ser
320				
Pro				
325				
Arg	Ile	Phe	Gln	Ser
330				
Ala	Gly	Ile	Thr	Asn
335				
Leu	Gln	Leu	Leu	
340				
Ala	Thr	Val	Ala	Val
345				
Gly	Val	Val	Lys	Thr
350				
Leu	Phe	Ile	Leu	Val
355				
Ala	Thr	Val	Ala	Val
360				
Gly	Arg	Arg	Pro	Leu
365				
Leu	Leu	Leu	Thr	Ser
370				
Val	Gly	Gly	Met	Ile
375				
Ile	Ala	Ile	Leu	Thr
380				
Met	Ser	Leu	Thr	
385				
Val	Ile	Asp	His	Ser
390				
His	His	Lys	Ile	Thr
395				
Trp	Ala	Ile	Ala	Leu
400				
Cys				
405				
Ile	Thr	Met	Val	Cys
410				
Ala	Val	Val	Ala	Ser
415				
Phe	Ser	Ile	Gly	Leu
420				
Arg	Leu	Arg	Leu	Arg
425				
Glu	Val	Phe	Pro	Leu
430				
Ala	Gln	Gly	Thr	Ser
435				
Met	Gly	Val	Ala	Val
440				
Asn	Arg	Val	Val	Ser
445				
Gly				
450				
Val	Ile	Ser	Ile	Phe
455				
Phe	Leu	Pro	Leu	Ser
460				
His	Lys	Ile	Thr	Thr
465				
Gly	Ala	Phe	Phe	Leu
470				
Phe	Gly	Gly	Ile	Ala
475				
Ile	Ile	Ala	Trp	Phe
480				
Phe	Leu	Thr	Phe	Leu
485				
Pro	Glu	Thr	Arg	Gly
490				
Asn	Glu	Asn	Met	
495				
His	Glu	Leu	Phe	Glu
500				
Asp	Phe	Arg	Trp	Arg
505				
Glu	Ser	Phe	Pro	Gly
510				
Asn	Gly	Asn		
515				
Lys	Ser	Asn	Asn	Asp
520				
Glu	Asn	Ser	Thr	Arg
525				
Lys	Gln	Ser	Asn	Gly
530				
Asp	Lys	Ser	Gln	Val

530

535

540

Thr Asn Asp Asn His  
545

<210> 31  
<211> 2777  
<212> DNA  
<213> Zea mays

<400> 31  
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ctgcttcgtg ttcttcacag gagccgggtga cctcggacga tatcttggag gacaagatgt 180  
cgggggctgt tcttgtcgcc atagtcgcct ccatcggcaa tctattgcag ggggtgggaca 240  
atgccaccat cgcagctgct gttctgtata taaagaagga atttcaattg caaaatgagc 300  
ccactgtgga gggactaatt gtgtcaatgt cacttatcgg cgccaccatc gttactacat 360  
tctccgggcc attatcagac tcgattggcc gacgccctat gcttattctc tcttcaattc 420  
tgtacttctt cagcggcctc atcatgctat ggtctcctaa tgtctatgtc ctgctgttgg 480  
cacgcttcgt agatggattt ggtattggct tggctgtcac gcttgtgcct ttgtacattt 540  
cagaaatagc cccttcggag attagaggtt tgctgaatac actaccacaa ttcagtggat 600  
caggaggaat gttcttgtca tactgcatgg tgtttgggat gtccctgtcg ccatcacccg 660  
attggagaat tatgcttggg gtgctcgca taccttcatt gttcttcttt ggtttgacaa 720  
tattttatct tcctgaatct ccaagatggc tcgttagcaa aggtcggatg gcagaggcaa 780  
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ccgaggcagc cgatgatctt gttactgacg gtgataagga acaaatcaca ctttatgggc 960  
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aaagagtcta cttgcaccaa gagggaggtc ctggctcaag aaggggctca attggtttcac 1560  
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ccaaatttgg tctcagctcg gcatcagcat ccattctgat cagttctctc actaccttac 1920  
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ctgcaaaagc ctaatttctt tggtagcttt gtgtgcaact attgcactgt aagttagaaa 2460  
cttgaagggg tttcaccaag aagctcggag aattactttg gatttgtgta aatgttaagg 2520  
gaacgaacat ctgctcatgc tcctcaaacg gtaaaaaaga gtccctcaat ggcaaatagg 2580  
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tcaagctatt caacgctggg tgttgctaga aatctttaga acaagatga taatgatctg 2700  
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aaaaaaaaaa aaaaaaa 2777

<210> 32  
<211> 800

10051909 Sequence Listing.txt

<212> PRT

<213> Zea mays

<400> 32

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Leu Asp Arg Arg Glu Arg Leu Leu Pro Ser Val Val Leu Ala Leu Pro
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Gly Pro Leu Pro Pro Ala Ser Cys Ser Ser Gln Glu Pro Val Thr Ser
          35          40          45
Asp Asp Ile Leu Glu Asp Lys Met Ser Gly Ala Val Leu Val Ala Ile
 50          55          60
Val Ala Ser Ile Gly Asn Leu Leu Gln Gly Trp Asp Asn Ala Thr Ile
 65          70          75          80
Ala Ala Ala Val Leu Tyr Ile Lys Lys Glu Phe Gln Leu Gln Asn Glu
          85          90          95
Pro Thr Val Glu Gly Leu Ile Val Ser Met Ser Leu Ile Gly Ala Thr
          100          105          110
Ile Val Thr Thr Phe Ser Gly Pro Leu Ser Asp Ser Ile Gly Arg Arg
          115          120          125
Pro Met Leu Ile Leu Ser Ser Ile Leu Tyr Phe Phe Ser Gly Leu Ile
          130          135          140
Met Leu Trp Ser Pro Asn Val Tyr Val Leu Leu Leu Ala Arg Phe Val
          145          150          155          160
Asp Gly Phe Gly Ile Gly Leu Ala Val Thr Leu Val Pro Leu Tyr Ile
          165          170          175
Ser Glu Ile Ala Pro Ser Glu Ile Arg Gly Leu Leu Asn Thr Leu Pro
          180          185          190
Gln Phe Ser Gly Ser Gly Gly Met Phe Leu Ser Tyr Cys Met Val Phe
          195          200          205
Gly Met Ser Leu Ser Pro Ser Pro Asp Trp Arg Ile Met Leu Gly Val
          210          215          220
Leu Ala Ile Pro Ser Leu Phe Phe Phe Gly Leu Thr Ile Phe Tyr Leu
          225          230          235          240
Pro Glu Ser Pro Arg Trp Leu Val Ser Lys Gly Arg Met Ala Glu Ala
          245          250          255
Lys Lys Val Leu Gln Lys Leu Arg Gly Lys Asp Asp Val Ser Gly Glu
          260          265          270
Leu Ser Leu Leu Leu Glu Gly Leu Glu Val Gly Gly Asp Thr Ser Ile
          275          280          285
Glu Glu Tyr Ile Ile Gly Pro Ala Thr Glu Ala Ala Asp Asp Leu Val
          290          295          300
Thr Asp Gly Asp Lys Glu Gln Ile Thr Leu Tyr Gly Pro Glu Glu Gly
          305          310          315          320

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10051909 Sequence Listing.txt

Gln	Ser	Trp	Ile	Ala 325	Arg	Pro	Ser	Lys	Gly 330	Pro	Ile	Met	Leu	Gly 335	Ser	
Val	Leu	Ser	Leu 340	Ala	Ser	Arg	His	Gly 345	Ser	Met	Val	Asn	Gln 350	Ser	Val	
Pro	Leu	Met 355	Asp	Pro	Ile	Val	Thr 360	Leu	Phe	Gly	Ser	Val 365	His	Glu	Asn	
Met	Pro 370	Gln	Ala	Gly	Gly	Ser 375	Met	Arg	Ser	Thr	Leu 380	Phe	Pro	Asn	Phe	
Gly 385	Ser	Met	Phe	Ser	Val 390	Thr	Asp	Gln	His	Ala 395	Lys	Asn	Glu	Gln	Trp 400	
Asp	Glu	Glu	Asn	Leu 405	His	Arg	Asp	Asp	Glu 410	Glu	Tyr	Ala	Ser	Asp 415	Gly	
Ala	Gly	Gly	Asp 420	Tyr	Glu	Asp	Asn	Leu 425	His	Ser	Pro	Leu	Leu 430	Ser	Arg	
Gln	Ala	Thr 435	Gly	Ala	Glu	Gly	Lys 440	Asp	Ile	Val	His	His 445	Gly	His	Arg	
Gly	Ser 450	Ala	Leu	Ser	Met	Arg 455	Arg	Gln	Thr	Leu	Leu 460	Gly	Glu	Gly	Gly	
Asp 465	Gly	Val	Ser	Ser	Thr 470	Asp	Ile	Gly	Gly	Gly 475	Trp	Gln	Leu	Ala	Trp 480	
Lys	Trp	Ser	Glu	Lys 485	Glu	Gly	Glu	Asn	Gly 490	Arg	Lys	Glu	Gly	Gly 495	Phe	
Lys	Arg	Val	Tyr 500	Leu	His	Gln	Glu	Gly 505	Val	Pro	Gly	Ser	Arg 510	Arg	Gly	
Ser	Ile	Val 515	Ser	Leu	Pro	Gly	Gly 520	Gly	Asp	Val	Phe	Glu 525	Gly	Ser	Glu	
Phe	Val 530	His	Ala	Ala	Ala	Leu 535	Val	Ser	Gln	Ser	Ala 540	Leu	Phe	Ser	Lys	
Gly 545	Leu	Ala	Glu	Pro	Arg 550	Met	Ser	Asp	Ala	Ala 555	Met	Val	His	Pro	Ser 560	
Glu	Val	Ala	Ala	Lys 565	Gly	Ser	Arg	Trp	Lys 570	Asp	Leu	Phe	Glu	Pro 575	Gly	
Val	Arg	Arg	Ala 580	Leu	Leu	Val	Gly	Val 585	Gly	Ile	Gln	Ile	Leu 590	Gln	Gln	
Phe	Ala	Gly 595	Ile	Asn	Gly	Val	Leu 600	Tyr	Tyr	Thr	Pro	Gln 605	Ile	Leu	Glu	
Gln	Ala 610	Gly	Val	Ala	Val	Ile 615	Leu	Ser	Lys	Phe	Gly 620	Leu	Ser	Ser	Ala	
Ser 625	Ala	Ser	Ile	Leu	Ile 630	Ser	Ser	Leu	Thr	Thr 635	Leu	Leu	Met	Leu	Pro 640	
Cys	Ile	Gly	Phe	Ala 645	Met	Leu	Leu	Met	Asp 650	Leu	Ser	Gly	Arg	Arg 655	Phe	

10051909 Sequence Listing.txt

Leu Leu Leu Gly Thr Ile Pro Ile Leu Ile Ala Ser Leu Val Ile Leu  
660 665 670

Val Val Ser Asn Leu Ile Asp Leu Gly Thr Leu Ala His Ala Leu Leu  
675 680 685

Ser Thr Val Ser Val Ile Val Tyr Phe Cys Cys Phe Val Met Gly Phe  
690 695 700

Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe Pro Thr Arg Val  
705 710 715 720

Arg Gly Leu Cys Ile Ala Ile Cys Ala Phe Thr Phe Trp Ile Gly Asp  
725 730 735

Ile Ile Val Thr Tyr Ser Leu Pro Val Met Leu Asn Ala Ile Gly Leu  
740 745 750

Ala Gly Val Phe Ser Ile Tyr Ala Val Val Cys Leu Ile Ser Phe Val  
755 760 765

Phe Val Phe Leu Lys Val Pro Glu Thr Lys Gly Met Pro Leu Glu Val  
770 775 780

Ile Thr Glu Phe Phe Ala Val Gly Ala Lys Gln Ala Ala Ala Lys Ala  
785 790 795 800

<210> 33  
<211> 2063  
<212> DNA  
<213> Zea mays

<400> 33

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cgctgcgctg	caacggggcgg	cggtgtcgtc	gcttcgtgga	gcggcgatcg	gagattgccg	180
gcggtcaacc	cctgcagcgt	gcggatgccg	acgggcaacg	atgggtgggtg	cgccggcctg	240
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gaagatatcc	cattggagaa	ggttcaagtt	aaatcctcag	gacatgttct	gccatatgtt	420
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gttagcacat	ccttggctgg	tgcaacacta	ggttctttta	ctgggggttc	tttggcagat	600
aaatttgggc	ggacaagaac	attcatcctg	gatgcagtc	cacttgctct	aggtgcattc	660
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gcctcgagaa	taagggccaa	ggctgtcgca	ttatctctag	gcatgcactg	ggtatctaac	1560
tttttcattg	gcctgtactt	cctgagtgtc	gtgagcaagt	ttgggatcag	caacgtgtat	1620
ctgggatttg	catcagtatg	tgcccttgca	gttctgtaca	tagctgggaa	tgtgggtcgag	1680

10051909 Sequence Listing.txt

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accaagggga gatcacttga agagattgaa agggagctaa gtgtagcaga atgatgtact 1740
tttgctagtc atgctgtggc gccgttttgg ttatcgagaa tgcaaccaag cgctcaaccg 1800
agcatccttg gacctggaga ctctttctag tttcatgtag ttttagaaat aagcgaacgg 1860
caagagtacc aatcttaggt gacttgggtg gggttgtgtc tgaaataagt gaattggatt 1920
gtagaatttc agaaataagt gaattggatt gtagaatttc aaaaagtgtg ttccccttaa 1980
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040
aaaaaaaaaa aaaaaaaaaa aaa                                     2063

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<210> 34  
 <211> 571  
 <212> PRT  
 <213> Zea mays

<400> 34

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Asn Leu Leu Leu Leu Ile Phe Gly Pro Phe His Phe Ile Arg Cys Thr
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Arg Arg Cys Arg Cys Gln His Gly Thr Ile Thr Thr Val Ile Lys Lys
          20          25          30
Met Met Arg Cys Ala Ala Thr Gly Gly Gly Cys Val Ala Ser Trp Ser
          35          40          45
Gly Asp Arg Arg Leu Pro Ala Val Asn Pro Cys Ser Val Arg Met Pro
          50          55          60
Thr Gly Asn Asp Gly Trp Cys Ala Gly Leu Arg Ser Arg Ala Ala Asp
 65          70          75          80
Leu Ala Gly Leu Glu Met Ala Asn Leu Arg Gly Gly Val Gly Gly Leu
          85          90          95
Phe Arg Ala Ser Pro Arg Tyr Gly Arg Leu Gln Ala Thr Ala Ala Val
          100          105          110
Asp Pro Glu Asp Ile Pro Leu Glu Lys Val Gln Val Lys Ser Ser Gly
          115          120          125
His Val Leu Pro Tyr Val Gly Val Ala Cys Leu Gly Ala Ile Leu Phe
          130          135          140
Gly Tyr His Leu Gly Val Val Asn Gly Ala Leu Glu Tyr Leu Ala Lys
          145          150          155          160
Asp Leu Gly Ile Ala Glu Asn Ala Val Leu Gln Gly Trp Val Val Ser
          165          170          175
Thr Ser Leu Ala Gly Ala Thr Leu Gly Ser Phe Thr Gly Gly Ser Leu
          180          185          190
Ala Asp Lys Phe Gly Arg Thr Arg Thr Phe Ile Leu Asp Ala Val Pro
          195          200          205
Leu Ala Leu Gly Ala Phe Leu Ser Ala Thr Ala Gln Asp Ile Arg Thr
          210          215          220
Met Ile Ile Gly Arg Leu Leu Ala Gly Ile Gly Ile Gly Val Ser Ser
          225          230          235          240
Ala Leu Val Pro Leu Tyr Ile Ser Glu Ile Ser Pro Thr Glu Ile Arg
          245          250          255

```

## 10051909 Sequence Listing.txt

Gly Thr Leu Gly Thr Val Asn Gln Leu Phe Ile Cys Ile Gly Ile Leu  
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 275 280 285  
 Arg Thr Met Phe Gly Ile Ala Val Val Pro Ser Ile Leu Leu Ala Val  
 290 295 300  
 Gly Met Ala Phe Ser Pro Glu Ser Pro Arg Trp Leu Phe Gln Gln Gly  
 305 310 315 320  
 Lys Val Thr Gln Ala Glu Leu Ala Val Lys Arg Leu Tyr Gly Lys Glu  
 325 330 335  
 Met Val Thr Glu Ile Met Phe Asp Leu Arg Ala Ser Gly Gln Ser Ser  
 340 345 350  
 Ser Glu Ser Glu Ala Gly Trp Phe Asp Leu Phe Ser Lys Arg Tyr Trp  
 355 360 365  
 Lys Val Val Ser Val Gly Ala Ala Leu Phe Leu Phe Gln Gln Leu Ala  
 370 375 380  
 Gly Ile Asn Ala Val Val Tyr Tyr Ser Thr Ser Val Phe Arg Ser Ala  
 385 390 395 400  
 Gly Ile Ala Ser Asp Val Ala Ala Ser Ala Leu Val Gly Ala Ala Asn  
 405 410 415  
 Val Phe Gly Thr Met Val Ala Ser Ser Leu Met Asp Lys Gln Gly Arg  
 420 425 430  
 Lys Ser Leu Leu Ile Thr Ser Phe Ser Gly Met Gly Ala Ser Met Leu  
 435 440 445  
 Leu Leu Ala Leu Ser Phe Thr Trp Lys Ala Leu Ala Pro Tyr Ser Gly  
 450 455 460  
 Thr Leu Ala Val Val Gly Thr Val Leu Tyr Val Leu Ser Phe Ala Leu  
 465 470 475 480  
 Gly Ala Gly Pro Val Pro Ala Leu Leu Leu Pro Glu Ile Phe Ala Ser  
 485 490 495  
 Arg Ile Arg Ala Lys Ala Val Ala Leu Ser Leu Gly Met His Trp Val  
 500 505 510  
 Ser Asn Phe Phe Ile Gly Leu Tyr Phe Leu Ser Val Val Ser Lys Phe  
 515 520 525  
 Gly Ile Ser Asn Val Tyr Leu Gly Phe Ala Ser Val Cys Ala Leu Ala  
 530 535 540  
 Val Leu Tyr Ile Ala Gly Asn Val Val Glu Thr Lys Gly Arg Ser Leu  
 545 550 555 560  
 Glu Glu Ile Glu Arg Glu Leu Ser Val Ala Glu  
 565 570

<210> 35  
 <211> 1953

10051909 Sequence Listing.txt

<212> DNA  
<213> Zea mays

<220>  
<221> unsure  
<222> (1584)  
<223> n = A, C, G or T

<400> 35  
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ggcggcagca acagaggcgg cgccggcgcc ggcgaggaga gcggcagcga ccacgacggg 180  
gtgctgcgga ggccgctgct caacacgggg agctgggtacc ggatgagctc gcggcagttc 240  
agctttgccc cggggacctc ctccatggcc gtcctgcgcg agtcccacgt ctccgccttc 300  
ctctgcacgc tcatcgtcgc gctcggcccc atccagttcg gcttcaccag cggcttctcc 360  
tccccgaccc aggacgccat gggtcgggac ctcaacctct ctatctccga gttctcggcg 420  
ttcggatcgc tgtccaacgt cggcggcatg gtcggggcga tcgccagcgg gcagatggcc 480  
gagtacattg gccgtaaagg gtcgttgatg attgctgcaa tcccaaatat catcggttgg 540  
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tttggtgtcg gcatcatatc ctacacggta ccggtataca tagcagagat atctcctcag 660  
aacatgaggg gagctcttgg ttctgtgaac cagttgtctg tgacctttgg catattcttg 720  
gcctatttgc tcggcatgtt tattccttgg agacttcttg ctgtgattgg agccttgccc 780  
tgcacaatgt tgattcctgg actattcttc attccagaat ctcccagatg gctggcaaag 840  
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atcacacag aagtgaatga tataaagagg gcagtggcat catcaagtaa gaggaccaca 960  
atcagttttc aagaattaaa ccaaaagaaa taccgcacgc cactacttct agggattggc 1020  
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aaggataaca ttacacagga ttctaactca tactacatct taacaatgat ctcccttggt 1320  
ggatttgtgt cttttgtcat taccttctcg tttggtatgg gtgccattcc atggctcatg 1380  
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ggaggcactt ttctctcgta catgggtgtg agcgcttca ccatcgtttt tggtgtcctt 1560  
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gagctaaagc aaaaagaagc taaaatttag tcactttata aactaaagtt ccaatcagga 1740  
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aggagctaga atttagtccc ttgttttagc ttatactcct tccatcctaa aaaaatatag 1860  
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acgtataaac tattcattaa aaaaaaaaaa aaa 1953

<210> 36  
<211> 553  
<212> PRT  
<213> Zea mays

<220>  
<221> UNSURE  
<222> (528)  
<223> Xaa = any amino acid

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20 25 30  
Glu Leu Arg Thr Arg Val Met Gly Gly Gly Ser Asn Arg Gly Gly Ala  
35 40 45

10051909 Sequence Listing.txt

Gly	Ala	Gly	Glu	Glu	Ser	Gly	Ser	Asp	His	Asp	Gly	Val	Leu	Arg	Arg
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Pro	Leu	Leu	Asn	Thr	Gly	Ser	Trp	Tyr	Arg	Met	Ser	Ser	Arg	Gln	Ser
65					70					75					80
Ser	Phe	Ala	Pro	Gly	Thr	Ser	Ser	Met	Ala	Val	Leu	Arg	Glu	Ser	His
				85					90					95	
Val	Ser	Ala	Phe	Leu	Cys	Thr	Leu	Ile	Val	Ala	Leu	Gly	Pro	Ile	Gln
			100					105					110		
Phe	Gly	Phe	Thr	Ser	Gly	Phe	Ser	Ser	Pro	Thr	Gln	Asp	Ala	Met	Val
		115					120					125			
Arg	Asp	Leu	Asn	Leu	Ser	Ile	Ser	Glu	Phe	Ser	Ala	Phe	Gly	Ser	Leu
	130					135					140				
Ser	Asn	Val	Gly	Gly	Met	Val	Gly	Ala	Ile	Ala	Ser	Gly	Gln	Met	Ala
145					150					155					160
Glu	Tyr	Ile	Gly	Arg	Lys	Gly	Ser	Leu	Met	Ile	Ala	Ala	Ile	Pro	Asn
				165					170					175	
Ile	Ile	Gly	Trp	Leu	Ala	Ile	Ser	Phe	Ala	Lys	Asp	Ala	Ser	Phe	Leu
			180					185					190		
Tyr	Met	Gly	Arg	Leu	Leu	Glu	Gly	Phe	Gly	Val	Gly	Ile	Ile	Ser	Tyr
		195					200					205			
Thr	Val	Pro	Val	Tyr	Ile	Ala	Glu	Ile	Ser	Pro	Gln	Asn	Met	Arg	Gly
	210					215					220				
Ala	Leu	Gly	Ser	Val	Asn	Gln	Leu	Ser	Val	Thr	Phe	Gly	Ile	Phe	Leu
225					230					235					240
Ala	Tyr	Leu	Leu	Gly	Met	Phe	Ile	Pro	Trp	Arg	Leu	Leu	Ala	Val	Ile
				245					250					255	
Gly	Ala	Leu	Pro	Cys	Thr	Met	Leu	Ile	Pro	Gly	Leu	Phe	Phe	Ile	Pro
			260					265					270		
Glu	Ser	Pro	Arg	Trp	Leu	Ala	Lys	Met	Asn	Leu	Thr	Glu	Asp	Cys	Glu
		275					280					285			
Thr	Ser	Leu	Gln	Val	Leu	Arg	Gly	Phe	Glu	Thr	Asp	Ile	Thr	Thr	Glu
	290					295					300				
Val	Asn	Asp	Ile	Lys	Arg	Ala	Val	Ala	Ser	Ser	Ser	Lys	Arg	Thr	Thr
305					310					315					320
Ile	Ser	Phe	Gln	Glu	Leu	Asn	Gln	Lys	Lys	Tyr	Arg	Thr	Pro	Leu	Leu
				325					330					335	
Leu	Gly	Ile	Gly	Leu	Leu	Val	Leu	Gln	Asn	Leu	Ser	Gly	Ile	Asn	Gly
			340					345					350		
Val	Leu	Phe	Tyr	Ala	Ser	Ser	Ile	Phe	Lys	Ala	Ala	Gly	Val	Thr	Asn
		355					360					365			
Ser	Asp	Leu	Ala	Thr	Cys	Ser	Leu	Gly	Ala	Ile	Gln	Val	Leu	Ala	Thr
	370					375					380				

10051909 Sequence Listing.txt

Gly Val Thr Thr Trp Leu Leu Asp Arg Ala Gly Arg Arg Ile Leu Leu  
385 390 395 400  
Ile Ile Ser Thr Ser Gly Met Thr Leu Cys Leu Leu Ala Val Ser Val  
405 410 415  
Val Phe Phe Leu Lys Asp Asn Ile Ser Gln Asp Ser Asn Ser Tyr Tyr  
420 425 430  
Ile Leu Thr Met Ile Ser Leu Val Gly Ile Val Ser Phe Val Ile Thr  
435 440 445  
Phe Ser Phe Gly Met Gly Ala Ile Pro Trp Leu Met Met Ser Glu Ile  
450 455 460  
Leu Pro Val Ser Ile Lys Ser Leu Gly Gly Ser Ile Ala Thr Leu Ala  
465 470 475 480  
Asn Trp Leu Thr Ser Phe Ala Ile Thr Met Thr Thr Asn Leu Met Leu  
485 490 495  
Thr Trp Ser Val Gly Gly Thr Phe Leu Ser Tyr Met Val Val Ser Ala  
500 505 510  
Phe Thr Ile Val Phe Val Val Leu Trp Val Pro Glu Thr Lys Gly Xaa  
515 520 525  
Asn Ser Arg Gly Asp Thr Ile Phe Val Ser Leu Ser Ile Gln Arg Gln  
530 535 540  
Leu Gln Trp Leu Pro Glu Cys Leu Ser  
545 550

<210> 37  
<211> 740  
<212> PRT  
<213> Oryza sativa

<400> 37  
Met Ala Gly Ala Val Leu Val Ala Ile Ala Ala Ser Ile Gly Asn Leu  
1 5 10 15  
Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val Leu Tyr Ile  
20 25 30  
Lys Lys Glu Phe Asn Leu Gln Ser Glu Pro Leu Ile Glu Gly Leu Ile  
35 40 45  
Val Ala Met Ser Leu Ile Gly Ala Thr Ile Ile Thr Thr Phe Ser Gly  
50 55 60  
Ala Val Ala Asp Ser Phe Gly Arg Arg Pro Met Leu Ile Ala Ser Ala  
65 70 75 80  
Val Leu Tyr Phe Val Ser Gly Leu Val Met Leu Trp Ala Pro Asn Val  
85 90 95  
Tyr Val Leu Leu Leu Ala Arg Leu Ile Asp Gly Phe Gly Ile Gly Leu  
100 105 110  
Ala Val Thr Leu Val Pro Leu Tyr Ile Ser Glu Thr Ala Pro Thr Asp

10051909 Sequence Listing.txt

115		120		125
Ile Arg Gly Leu Leu Asn Thr Leu Pro Gln Phe Ser Gly Ser Gly Gly	130	135	140	
Met Phe Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Met Pro Gln	145	150	155	160
Pro Asp Trp Arg Ile Met Leu Gly Val Leu Ser Ile Pro Ser Leu Ile	165	170	175	
Tyr Phe Ala Leu Thr Ile Phe Tyr Leu Pro Glu Ser Pro Arg Trp Leu	180	185	190	
Val Ser Lys Gly Arg Met Ala Glu Ala Lys Arg Val Leu Gln Gly Leu	195	200	205	
Arg Gly Arg Glu Asp Val Ser Gly Glu Met Ala Leu Leu Val Glu Gly	210	215	220	
Leu Gly Val Gly Lys Asp Thr Lys Ile Glu Glu Tyr Ile Ile Gly Pro	225	230	235	240
Asp Asp Glu Leu Ala Asp Glu Gly Leu Ala Pro Asp Pro Glu Lys Ile	245	250	255	
Lys Leu Tyr Gly Pro Glu Glu Gly Leu Ser Trp Val Ala Arg Pro Val	260	265	270	
His Gly Gln Ser Ala Leu Gly Ser Ala Leu Gly Leu Ile Ser Arg His	275	280	285	
Gly Ser Met Val Ser Gln Gly Lys Pro Leu Val Asp Pro Val Val Thr	290	295	300	
Leu Phe Gly Ser Val His Glu Lys Met Pro Glu Ile Met Gly Ser Met	305	310	315	320
Arg Ser Thr Leu Phe Pro Asn Phe Gly Ser Met Phe Ser Val Ala Glu	325	330	335	
Gln Gln Gln Ala Lys Gly Asp Trp Asp Ala Glu Ser Gln Arg Glu Gly	340	345	350	
Glu Asp Tyr Gly Ser Asp His Gly Gly Asp Asp Ile Glu Asp Ser Leu	355	360	365	
Gln Ser Pro Leu Ile Ser Arg Gln Ala Thr Ser Val Glu Gly Lys Glu	370	375	380	
Ile Ala Ala Pro His Gly Ser Ile Met Gly Ala Val Gly Arg Ser Ser	385	390	395	400
Ser Leu Met Gln Gly Gly Glu Ala Val Ser Ser Met Gly Ile Gly Gly	405	410	415	
Gly Trp Gln Leu Ala Trp Lys Trp Thr Glu Arg Glu Gly Ala Asp Gly	420	425	430	
Glu Lys Glu Gly Gly Phe Gln Arg Ile Tyr Leu His Glu Glu Gly Val	435	440	445	
Thr Gly Asp Arg Arg Gly Ser Ile Leu Ser Leu Pro Gly Gly Asp Val				

10051909 Sequence Listing.txt

450		455		460	
Pro 465	Pro Gly	Gly Glu	Phe 470	Val Gln	Ala Ala
	Ala Leu	Tyr Ser	Lys 485	Glu Leu	Met Glu
				Gln 490	Arg Leu
					Ala Gly
					Pro 495
Met 500	Val His	Pro Ser	Gln 505	Ala Val	Lys Gly
					Pro Lys
					Trp 510
					Ala Asp
Leu 515	Phe Glu	Pro Gly	Val Lys	His 520	Ala Leu
					Phe Val
					Gly 525
					Ile Gly
					Ile Thr
Gln 530	Ile Leu	Gln Gln	Phe 535	Ala Gly	Ile Asn
					Gly Val
					Leu 540
					Tyr Tyr
					Thr Thr
Pro 545	Gln Ile	Leu Glu	Gln 550	Ala Gly	Val Gly
					Val 555
					Leu Leu
					Ala Asn
					Ile 560
Gly 565	Leu Ser	Ser Ser	Ser 570	Ala Ser	Ile Leu
					Ile 575
					Ser Gly
					Leu Thr
					Thr Thr
Leu 580	Leu Met	Pro Ser	Ile Gly	Ile 585	Ala Met
					Arg Leu
					Met 590
					Asp Met
Ser 595	Gly Arg	Arg Phe	Leu Leu	Leu 600	Ala Thr
					Ile 605
					Pro Leu
					Ile Val
Ala 610	Leu Ala	Ile Leu	Ile Leu	Val 615	Asn Ile
					Leu Asp
					Val 620
					Gly Thr
					Met Met
Val 625	His Ala	Ser Leu	Ser 630	Thr Val	Ser Val
					Ile 635
					Leu Tyr
					Phe Cys
					Phe 640
Phe 645	Val Met	Gly Phe	Gly Pro	Ile Pro	Asn Ile
					Leu Cys
					Ala Glu
					Ile 655
Phe 660	Pro Thr	Thr Val	Arg Gly	Ile Cys	Ile Ala
					Ile 670
					Cys Ala
					Leu Thr
Phe 675	Trp Ile	Gly Asp	Ile Ile	Val 680	Thr Tyr
					Thr 685
					Leu Pro
					Val Met
					Leu Leu
Asn 690	Ala Ile	Gly Leu	Ala Gly	Val 695	Phe Gly
					Ile Tyr
					Ala Val
					Val Cys
Ile 705	Leu Ala	Phe Leu	Phe 710	Val Phe	Met Lys
					Val 715
					Pro Glu
					Thr Lys
					Gly 720
Met 725	Pro Leu	Glu Val	Ile Thr	Glu Phe	Phe Ser
					Val 730
					Gly Ala
					Lys 735
					Gln Gln
Ala 740	Lys Glu	Asp			

<210> 38  
 <211> 501  
 <212> PRT  
 <213> Oryza sativa

<400> 38

10051909 Sequence Listing.txt

Met	Ser	Phe	Arg	Gly	Glu	Glu	Ser	Gly	Gly	Glu	Asp	Gly	Gly	Arg	Thr
1				5				10						15	
Ala	Ser	Ala	Ser	Asp	Leu	Arg	Lys	Pro	Phe	Leu	His	Thr	Gly	Ser	Trp
			20					25					30		
Tyr	Lys	Met	Ser	Ser	Ala	Gly	Gly	Gly	Gly	Gly	Met	Gly	Ser	Arg	Leu
		35					40					45			
Gly	Ser	Ser	Ala	Tyr	Ser	Leu	Arg	Asp	Ser	Ser	Val	Ser	Ala	Val	Leu
	50					55					60				
Cys	Thr	Leu	Ile	Val	Ala	Leu	Gly	Pro	Ile	Gln	Phe	Gly	Phe	Thr	Cys
65					70					75					80
Gly	Phe	Ser	Ser	Pro	Thr	Gln	Asp	Ala	Ile	Ile	Ser	Asp	Leu	Gly	Leu
				85					90					95	
Thr	Leu	Ser	Glu	Phe	Ser	Leu	Phe	Gly	Ser	Leu	Ser	Asn	Val	Gly	Ala
			100					105					110		
Met	Val	Gly	Ala	Ile	Ala	Ser	Gly	Gln	Ile	Ala	Glu	Tyr	Ile	Gly	Arg
		115					120					125			
Lys	Gly	Ser	Leu	Met	Ile	Ala	Ala	Ile	Pro	Asn	Ile	Ile	Gly	Trp	Leu
	130					135					140				
Ala	Ile	Ser	Phe	Ala	Lys	Asp	Ser	Ser	Phe	Leu	Phe	Met	Gly	Arg	Leu
145					150					155					160
Leu	Glu	Gly	Phe	Gly	Val	Gly	Val	Ile	Ser	Tyr	Val	Val	Pro	Val	Tyr
				165					170					175	
Ile	Ala	Glu	Ile	Ala	Pro	Gln	Thr	Met	Arg	Gly	Ala	Leu	Gly	Ser	Val
			180					185					190		
Asn	Gln	Leu	Ser	Val	Thr	Ile	Gly	Ile	Leu	Leu	Ala	Tyr	Leu	Leu	Gly
		195					200					205			
Met	Phe	Val	Pro	Trp	Arg	Ile	Leu	Ser	Val	Leu	Gly	Ile	Leu	Pro	Cys
	210					215					220				
Ser	Ile	Leu	Ile	Pro	Gly	Leu	Phe	Phe	Ile	Pro	Glu	Ser	Pro	Arg	Trp
225					230					235					240
Leu	Ala	Lys	Met	Gly	Lys	Met	Glu	Asp	Phe	Glu	Ser	Ser	Leu	Gln	Val
				245					250					255	
Leu	Arg	Gly	Phe	Glu	Thr	Asp	Ile	Ala	Val	Glu	Val	Asn	Glu	Ile	Lys
			260					265					270		
Arg	Ser	Val	Gln	Ser	Ser	Arg	Arg	Arg	Thr	Thr	Ile	Arg	Phe	Ala	Asp
		275					280					285			
Ile	Lys	Gln	Lys	Arg	Tyr	Ser	Val	Pro	Leu	Met	Val	Gly	Ile	Gly	Leu
	290					295					300				
Leu	Val	Leu	Gln	Gln	Leu	Ser	Gly	Val	Asn	Gly	Ile	Leu	Phe	Tyr	Ala
305					310					315					320
Ala	Ser	Ile	Phe	Lys	Ala	Ala	Gly	Leu	Thr	Asn	Ser	Asn	Leu	Ala	Thr
				325					330					335	

10051909 Sequence Listing.txt

Phe Gly Leu Gly Val Val Gln Val Val Ala Thr Gly Val Thr Thr Trp  
340 345 350  
Leu Thr Asp Lys Ala Gly Arg Arg Leu Leu Leu Ile Ile Ser Thr Thr  
355 360 365  
Gly Met Thr Ile Thr Leu Val Val Val Ser Val Ser Phe Phe Val Lys  
370 375 380  
Asp Asn Ile Thr Asn Gly Ser His Leu Tyr Ser Val Met Ser Met Leu  
385 390 395 400  
Ser Leu Val Gly Leu Val Ala Phe Val Ile Ser Phe Ser Leu Gly Leu  
405 410 415  
Gly Ala Ile Pro Trp Ile Ile Met Ser Glu Ile Leu Pro Val Asn Ile  
420 425 430  
Lys Ser Leu Ala Gly Ser Val Ala Thr Leu Ala Asn Trp Leu Thr Ala  
435 440 445  
Trp Leu Ile Thr Met Thr Ala Ser Leu Met Leu Ser Trp Ser Asn Gly  
450 455 460  
Gly Thr Phe Ala Ile Tyr Ala Ala Val Cys Ala Gly Thr Leu Val Phe  
465 470 475 480  
Val Cys Leu Trp Val Pro Glu Thr Lys Gly Arg Thr Leu Glu Glu Ile  
485 490 495  
Ala Phe Ser Phe Arg  
500

<210> 39  
<211> 7  
<212> PRT  
<213> Artificial

<220>  
<223> Conserved sequence element disclosed in the sequence alignment of Figure 2.

<400> 39

Pro Glu Ser Pro Arg Trp Leu  
1 5

<210> 40  
<211> 5  
<212> PRT  
<213> Artificial

<220>  
<223> Conserved sequence element disclosed in the sequence alignment of Figure 2.

<220>  
<221> misc\_feature  
<222> (4)..(4)  
<223> Xaa = any amino acid

10051909 Sequence Listing.txt

<400> 40

Pro Glu Thr Xaa Gly  
1 5

<210> 41

<211> 12

<212> PRT

<213> Artificial

<220>

<223> Conserved sequence element disclosed in the sequence alignment of Figure 2.

<220>

<221> misc\_feature

<222> (5)..(5)

<223> Xaa = any amino acid

<400> 41

Leu Gly Tyr Asp Xaa Ile Gly Val Met Ser Gly Ala  
1 5 10

<210> 42

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Conserved sequence element disclosed in the sequence alignment of Figure 2.

<220>

<221> misc\_feature

<222> (3)..(5)

<223> Xaa = any amino acid

<220>

<221> misc\_feature

<222> (7)..(7)

<223> Xaa = any amino acid

<400> 42

Gly Arg Xaa Xaa Xaa Gly Xaa Gly Val Gly  
1 5 10

<210> 43

<211> 6

<212> PRT

<213> Artificial

<220>

<223> Conserved sequence element disclosed in the sequence alignment of Figure 2.

<400> 43

10051909 Sequence Listing.txt

Gly Ile His Phe Phe Gln  
1 5

<210> 44  
<211> 6  
<212> PRT  
<213> Artificial

<220>  
<223> Conserved sequence element disclosed in the sequence alignment of Figure 2.

<220>  
<221> misc\_feature  
<222> (3)..(3)  
<223> Xaa = any amino acid

<220>  
<221> misc\_feature  
<222> (5)..(5)  
<223> Xaa = any amino acid

<400> 44

Phe Ser Xaa Gly Xaa Gly  
1 5

<210> 45  
<211> 18  
<212> PRT  
<213> Artificial

<220>  
<223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

<220>  
<221> misc\_feature  
<222> (5)..(5)  
<223> Xaa = any amino acid

<220>  
<221> misc\_feature  
<222> (8)..(8)  
<223> Xaa = any amino acid

<220>  
<221> misc\_feature  
<222> (14)..(14)  
<223> Xaa = any amino acid

<400> 45

Asp Gly Phe Gly Xaa Gly Leu Xaa Val Thr Leu Val Pro Xaa Tyr Ile  
1 5 10 15

Ser Glu

10051909 Sequence Listing.txt

<210> 46  
 <211> 25  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

<220>  
 <221> misc\_feature  
 <222> (7)..(7)  
 <223> Xaa = any amino acid

<220>  
 <221> misc\_feature  
 <222> (9)..(10)  
 <223> Xaa = any amino acid

<400> 46

Asn Thr Leu Pro Gln Phe Xaa Gly Xaa Xaa Gly Gly Met Phe Leu Ser  
 1 5 10 15

Tyr Cys Met Val Phe Gly Met Ser Leu  
 20 25

<210> 47  
 <211> 10  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Xaa = any amino acid

<400> 47

Met Leu Gly Val Leu Xaa Ile Pro Ser Leu  
 1 5 10

<210> 48  
 <211> 13  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

10051909 Sequence Listing.txt

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Xaa = any amino acid  
 <400> 48

Arg Trp Leu Val Ser Lys Gly Arg Met Xaa Glu Ala Lys  
 1 5 10

<210> 49  
 <211> 6  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

<400> 49

Glu Tyr Ile Ile Gly Pro  
 1 5

<210> 50  
 <211> 12  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

<220>  
 <221> misc\_feature  
 <222> (3)..(3)  
 <223> Xaa = any amino acid

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Xaa = any amino acid

<400> 50

Asp Pro Xaa Val Thr Leu Phe Gly Ser Xaa His Glu  
 1 5 10

<210> 51  
 <211> 16  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

<220>

10051909 Sequence Listing.txt

<221> misc\_feature  
<222> (6)..(6)  
<223> Xaa = any amino acid

<220>  
<221> misc\_feature  
<222> (10)..(10)  
<223> Xaa = any amino acid

<400> 51

Gly Ser Met Arg Ser Xaa Leu Phe Pro Xaa Phe Gly Ser Met Phe Ser  
1 5 10 15

<210> 52  
<211> 11  
<212> PRT  
<213> Artificial

<220>  
<223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

<220>  
<221> misc\_feature  
<222> (7)..(7)  
<223> Xaa = any amino acid

<400> 52

Ile Gly Gly Gly Trp Gln Xaa Ala Trp Lys Trp  
1 5 10

<210> 53  
<211> 23  
<212> PRT  
<213> Artificial

<220>  
<223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

<220>  
<221> misc\_feature  
<222> (5)..(5)  
<223> Xaa = any amino acid

<220>  
<221> misc\_feature  
<222> (20)..(20)  
<223> Xaa = any amino acid

<400> 53

Leu Gln Gln Phe Xaa Gly Ile Asn Gly Val Leu Tyr Tyr Thr Pro Gln  
1 5 10 15

Ile Leu Glu Xaa Ala Gly Val

20

<210> 54  
 <211> 19  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

<220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> Xaa = any amino acid

<220>  
 <221> misc\_feature  
 <222> (9)..(9)  
 <223> Xaa = any amino acid

<220>  
 <221> misc\_feature  
 <222> (13)..(13)  
 <223> Xaa = any amino acid

<220>  
 <221> misc\_feature  
 <222> (17)..(17)  
 <223> Xaa = any amino acid

<400> 54

Leu	Met	Asp	Xaa	Ser	Gly	Arg	Arg	Xaa	Leu	Leu	Leu	Xaa	Thr	Ile	Pro
1				5					10					15	

Xaa Leu Ile

<210> 55  
 <211> 34  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

<220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> Xaa = any amino acid

<220>  
 <221> misc\_feature  
 <222> (12)..(12)  
 <223> Xaa = any amino acid

10051909 Sequence Listing.txt

<220>  
 <221> misc\_feature  
 <222> (18)..(18)  
 <223> Xaa = any amino acid

<220>  
 <221> misc\_feature  
 <222> (24)..(24)  
 <223> Xaa = any amino acid

<400> 55

Tyr Phe Cys Xaa Phe Val Met Gly Phe Gly Pro Xaa Pro Asn Ile Leu  
 1 5 10 15

Cys Xaa Glu Ile Phe Pro Thr Xaa Val Arg Gly Leu Cys Ile Ala Ile  
 20 25 30

Cys Ala

<210> 56  
 <211> 17  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Conserved sequence element disclosed in the sequence alignment of Figure 1.

<220>  
 <221> misc\_feature  
 <222> (14)..(14)  
 <223> Xaa = any amino acid

<400> 56

Lys Val Pro Glu Thr Lys Gly Met Pro Leu Glu Val Ile Xaa Glu Phe  
 1 5 10 15

Phe